

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 17:52:00 ; Search time 78 Seconds
(without alignments)
876.379 Million cell updates/sec

Title: US-09-742-684A-16

Perfect score: 2770

Sequence: 1 MGAALKAFANFLISCSGA.....IVTVVTWVTVNDPPPKSSSL 513

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2770	100.0	513	AAW93211	Human activin rece
2	2770	100.0	513	AAW93211	Human activin rece
3	2770	100.0	513	AAW93211	Protein of a human
4	2765	99.8	513	AAW93211	Human activin rece
5	2763	99.7	513	AAW93211	Mouse activin rece
6	2763	99.7	513	AAW93211	Mouse activin rece
7	2763	99.7	513	AAW93211	Mouse activin rece
8	2763	99.7	513	AAW93211	Protein of a mouse
9	2758	99.6	513	AAW93211	Mouse activin rece
10	2744	99.1	521	AAW93211	Mouse activin rece

11	1971.5	71.2	510	20	AAW93204	Xenopus activin re
12	1971.5	71.2	510	22	AAW93206	Xenopus activin re
13	1971.5	71.2	510	23	AAW93206	Protein of a Xenop
14	1968.5	71.1	510	23	AAW93206	Xenopus activin re
15	1935	69.9	512	20	AAW93206	Mouse ActRIIB2 rec
16	1934	69.8	536	20	AAW93206	Mouse ActRIIB2 rec
17	1931	69.7	536	21	AAW93206	Human activin typ
18	1923	69.4	504	20	AAW93206	Mouse ActRIIB3 rec
19	1922	69.4	528	20	AAW93206	Mouse ActRIIB3 rec
20	1915.5	69.2	513	21	AAW93206	Rat activin type I
21	1150.5	41.5	516	22	AAW93206	Drosophila melanog
22	1147.5	41.4	516	19	AAW93206	Drosophila morphog
23	1147.5	41.4	516	20	AAW93206	Drosophila morphog
24	1147.5	41.4	516	21	AAW93206	Drosophila morphog
25	777.5	28.1	1038	17	AAW93206	Human BMP receptor
26	777.5	28.1	1040	23	AAW93206	Human BMPR-2 mutan
27	775.5	28.0	567	14	AAW93206	TGF-beta1 receptor
28	775.5	28.0	567	21	AAW93206	Human Transforming
29	775.5	28.0	567	22	AAW93206	Type II TGFbeta re
30	775.5	28.0	567	23	AAW93206	Human truncated BM
31	775.5	28.0	582	17	AAW93206	Truncated bone mor
32	775.5	28.0	582	17	AAW93206	Human BMPR-2 mutan
33	775.5	28.0	673	23	AAW93206	Human BMPR-2 mutan
34	775.5	28.0	801	23	AAW93206	Human BMPR-2 mutan
35	775.5	28.0	815	23	AAW93206	Human bone morphog
36	775.5	28.0	870	23	AAW93206	Human bone morphog
37	775.5	28.0	872	23	AAW93206	Human bone morphog
38	775.5	28.0	898	23	AAW93206	Human BMPR-2 mutan
39	775.5	28.0	898	23	AAW93206	Human bone morphog
40	775.5	28.0	1038	17	AAW93206	Human TGF-beta typ
41	775.5	28.0	1038	17	AAW93206	Bone morphogenetic
42	775.5	28.0	1038	17	AAW93206	Human BMP receptor
43	775.5	28.0	1038	23	AAW93206	Reference sequence
44	775.5	28.0	1038	23	AAW93206	Polymorphic varian
45	775.5	28.0	1038	23	AAW93206	Polymorphic varian

ALIGNMENTS

RESULT 1
AAW93211
ID AAW93211 standard; Protein; 513 AA.

AC AAW93211;

DT 27-MAY-1999 (first entry)

DE Human activin receptor pre-cursor protein.

DE Activin receptor; activin/TGF-superfamily; receptor protein; function;
DE activity; modulate; treatment; carcinogenesis; wound healing; fertility;
DE immune system disorder; central nervous system disorder; human;
DE reproductive system.

OS Homo sapiens.

PN US5885794-A.

PD 23-MAR-1999.

PF 02-SEP-1994; 94US-0300584.

PR 08-MAY-1992; 92US-0880220.

PR 10-MAY-1991; 91US-0698709.

PR 09-OCT-1991; 91US-0773229.

PR 02-SEP-1994; 94US-0300584.

PA (SALK) SALK INST BIOLOGICAL STUDIES.

PI Mathews LS, Vale WW;

XX WPI; 1999-228534/19.

DR

DR N-PSDB; AAX22685.

XX Isolated nucleic acid molecules encoding vertebrate activin receptor

PT polypeptides - useful as probes for detecting similar sequences and

PT for investigating the function of the receptor in conditions such as

PT carcinogenesis, wound healing and disorders of the immune, central

PT nervous and reproductive systems

XX Disclosure; Page -: 28pp; English.

XX This sequence represents a human activin receptor polypeptide. The

CC nucleic acid molecules of the invention are useful as probes for the

CC identification of additional members of the activin/TGF-superfamily of

CC receptor proteins, and the coding sequences can be used for the

CC recombinant expression of the receptor proteins or functional fragments

CC of them. They may also be used to study the function and activity of

CC activin receptor polypeptides in cells and to identify agents which will

CC modulate activin receptor expression and activity for use in treating

CC conditions such as carcinogenesis, wound healing, disorders of the

CC immune or central nervous systems and especially the reproductive system

CC (where they may be used to control fertility in humans, domestic and

CC commercial animals).

CC NOTE: This sequence does not appear in the specification but has been

CC created from the mouse activin receptor sequence (represented in

CC AAW93203) as described in the specification.

XX

XX Sequence 513 AA;

SQ Query Match 100.0%; Score 2770; DB 20; Length 513;

Best Local Similarity 100.0%; Pred. No. 2.2e-271;

Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKRRHC 60

Db 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKRRHC 60

QY 61 FATWKNISGSIEIVKQGCWLLDDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120

Db 61 FATWKNISGSIEIVKQGCWLLDDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120

QY 121 EYVQTSNPVTPPKPYNYLLYSLVPLMLIAGIVICAFWYRHHKMAYPVVLVPTQDGP 180

Db 121 EYVQTSNPVTPPKPYNYLLYSLVPLMLIAGIVICAFWYRHHKMAYPVVLVPTQDGP 180

QY 181 PPPSPILGLKPLQLEVKARGFGVCWKAQLLNEYVAVKFIPIQDKSQWNEYEYISLP 240

Db 181 PPPSPILGLKPLQLEVKARGFGVCWKAQLLNEYVAVKFIPIQDKSQWNEYEYISLP 240

QY 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300

QY 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300

QY 301 AYLHEDIPLGDKGHPATSHRDIKSNVLLKNNLTACIADFGLALKFPAKSGAGDTGQV 360

Db 301 AYLHEDIPLGDKGHPATSHRDIKSNVLLKNNLTACIADFGLALKFPAKSGAGDTGQV 360

QY 361 GTRRYMAPEVLGAINFORDAFLRDMYAMGLVLMELASRCTAADGPVDEYMLPFEERIG 420

Db 361 GTRRYMAPEVLGAINFORDAFLRDMYAMGLVLMELASRCTAADGPVDEYMLPFEERIG 420

QY 421 QHPSLEDQEVVYHKKRVLRYDQKAGMAMLCETIEECWHDHDAEALRSAGCVGERIT 480

Db 421 QHPSLEDQEVVYHKKRVLRYDQKAGMAMLCETIEECWHDHDAEALRSAGCVGERIT 480

QY 481 QMORLTNIITTEDIVTVTMVTNVDFPPKESL 513

Db 481 QMORLTNIITTEDIVTVTMVTNVDFPPKESL 513

RESULT 2

AAB47027

ID AAB47027 standard; Protein; 513 AA.

XX

AC AAB47027;

XX 29-MAR-2001 (first entry)

XX Human activin receptor.

DE

XX Mouse; human; rat; Xenopus; activin receptor; ligand binding domain;

KW transmembrane domain; receptor domain; serine kinase; TGF-beta;

KW transforming growth factor-beta; carcinogenesis; cancer;

KW wound healing.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Peptide 1..20

FT /note= "Secretion signal peptide"

XX US6162896-A.

XX 19-DEC-2000.

XX 07-JUN-1995; 95US-0476123.

XX 08-MAY-1992; 92US-0880220.

PR 10-MAY-1991; 91US-0698709.

PR 09-OCT-1991; 91US-0773229.

PR 02-SEP-1994; 94US-0300584.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Tsuchida K, Vale WW, Mathews LW;

XX WPI; 2001-090408/10.

DR N-PSDB; AAC85299.

XX Novel vertebrate activin receptor having extracellular ligand binding

PT domain, transmembrane domain and intracellular serine/threonine kinase

PT domain is useful for diagnosing and treating e.g. carcinogenesis, wound

PT healing

XX Claim 11; Page -: 33pp; English.

XX This sequence shows a human-derived activin receptor. The activin

CC receptors of the invention comprise three distinct domains: an

CC extracellular, ligand binding domain, a hydrophobic, transmembrane

CC domain and an intracellular, receptor domain having serine kinase-like

CC activity. These proteins have binding affinity for at least one

CC member of the activin/TGF-beta superfamily of polypeptide growth

CC factors. The activin receptor proteins of the invention can be

CC employed for a variety of therapeutic uses, e.g. to block receptors.

CC The presence of the soluble proteins will compete with functional

CC ligand for the receptor, preventing the formation of a functional

CC receptor-ligand complex, thereby blocking the normal regulatory

CC action of the complex. The receptor proteins are useful for the

CC diagnosis and therapeutic management of carcinogenesis, wound healing,

CC disorders of the immune, reproductive, or central nervous systems.

CC Note: This sequence is not shown in the specification but is derived

CC from the mouse-derived activin receptor sequence (see AAB47025).

XX

SQ Sequence 513 AA;

Query Match 100.0%; Score 2770; DB 22; Length 513;

Best Local Similarity 100.0%; Pred. No. 2.2e-271;

Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKRRHC 60

Db 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKRRHC 60

QY 61 FATWKNISGSIEIVKQGCWLLDDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120

Db 61 FATWKNISGSIEIVKQGCWLLDDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120

Db 481 QMRLTNIITTEDIVTVTVMTNVDPPKESL 513

RESULT 4
AAR29583
ID AAR29583 standard; Protein; 513 AA.

XX AAR29583;
XX 19-APR-1993 (first entry)
XX Human activin receptor.

XX Activin receptor; mouse; Xenopus; human; extracellular; ligand binding;
XX hydrophobic; trans-membrane; intracellular; receptor; domain;
XX serine kinase-like; activity; probe; superfamily; secretin signal;
XX golgi membrane; diagnosis; treatment; activin-dependent tumour; brain;
XX neuron; abortion; twinning; wound healing; TGF-beta; immune response;
XX liver regeneration.

XX Homo sapiens.

XX WO9220793-A;
XX 26-NOV-1992.
XX 08-MAY-1992; 92WO-US03825.
XX 10-MAY-1991; 91US-0698709.
XX 09-OCT-1991; 91US-0773229.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Mathews LS, Vale WW;
XX WPI; 1992-415771/50.
XX N-PSDB; AAQ31912.

XX New member of activin-transforming growth factor beta
XX super-family - for diagnosis and treatment of cancer and
XX disorders of the immune, reproductive or central nervous system

XX Disclosure; Page 40; 68pp; English.

XX The sequences given in AAR29581-83 represent activin receptors from
XX mouse, xenopus and human respectively. Each of these proteins
XX comprise three distinct domains: an extracellular, ligand binding
XX domain, a hydrophobic, trans-membrane domain and an intracellular,
XX receptor domain having serine kinase-like activity. The DNA sequences
XX encoding these proteins can be used as probes for the identification
XX of additional members of this superfamily of receptor molecules. The
XX proteins may further comprise a second hydrophobic domain at the amino
XX terminal which comprises a secretion signal sequence which promotes
XX the intracellular transport of the initially expressed receptor
XX protein across the golgi membrane. These receptor proteins can be
XX used to develop agents for the diagnosis and/or treatment of brain
XX activin-dependent tumours, for enhancing the survival of brain
XX neurons, for inducing abortion or twinning in livestock, for
XX stimulating wound healing, for suppression of growth of TGF-beta
XX sensitive tumours, for suppressing immune response, for promoting
XX liver regeneration and for stimulating some immune responses.

XX Sequence 513 AA;

Query Match 99.88; Score 2765; DB 13; Length 513;
Best Local Similarity 99.88; Pred. No. 7.1e-271;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGAALAFVFLISCSGAILGRSETQECLEFFNANWEKDRNTGTGPEYCGDKRRHC 60
Db 1 MGAALAFVFLISCSGAILGRSETQECLEFFNANWEKDRNTGTGPEYCGDKRRHC 60

QY 61 FATWKNISGSIIVKQGCWLDINCIDRTDCVEKKDSEVIFCCCEGNMCNEKFSYFFPM 120
Db 61 FATWKNISGSIIVKQGCWLDINCIDRTDCVEKKDSEVIFCCCEGNMCNEKFSYFFPM 120
QY 121 EVTQPTSNPTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVVLVPTQDPGP 180
Db 121 EVTQPTSNPTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVVLVPTQDPGP 180
QY 181 PPPSPLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIPIQDKQSQWNEYEYISLPG 240
Db 181 PPPSPLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIPIQDKQSQWNEYEYISLPG 240
QY 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKNVWSNQLCHIAETMARGL 300
Db 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKNVWSNQLCHIAETMARGL 300
QY 301 AYLEDIPCLGKHGHPAISHRDIKSKNVLKNNLTACIADFGALKFAGKSAGDTHGQV 360
Db 301 AYLEDIPCLGKHGHPAISHRDIKSKNVLKNNLTACIADFGALKFAGKSAGDTHGQV 360
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAADGPVDEYMLPFEETIG 420
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAADGPVDEYMLPFEETIG 420
QY 421 QHPSLEDQEVVYVHKRPVLDYQWKHAGMAMLCETIEECHDHDAAEARSAGCVGERIT 480
Db 421 QHPSLEDQEVVYVHKRPVLDYQWKHAGMAMLCETIEECHDHDAAEARSAGCVGERIT 480
QY 481 QMRLTNIITTEDIVTVTVMTNVDPPKESL 513
Db 481 QMRLTNIITTEDIVTVTVMTNVDPPKESL 513

RESULT 5

AAW93203
ID AAW93203 standard; Protein; 513 AA.

XX AAW93203;
XX 27-MAY-1999 (first entry)

XX Mouse activin receptor pre-cursor protein.

XX Activin receptor; activin/TGF-superfamily; receptor protein; function;
XX activity; modulate; treatment; carcinogenesis; wound healing; fertility;
XX immune system disorder; central nervous system disorder; mouse;
XX reproductive system.

XX Mus sp.

XX US5885794-A.

XX 23-MAR-1999.

XX 02-SEP-1994; 94US-0300584.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Mathews LS, Vale WW;

XX WPI; 1999-228534/19.

XX N-PSDB; AAX22683.

PT Isolated nucleic acid molecules encoding vertebrate activin receptor
PT polypeptides - useful as probes for detecting similar sequences and
PT for investigating the function of the receptor in conditions such as
PT carcinogenesis, wound healing and disorders of the immune, central
PT nervous and reproductive systems

XX Claim 29; Column 25-28; 28pp; English.

XX This sequence represents a mouse activin receptor polypeptide. The

XX nucleic acid molecules of the invention are useful as probes for the

XX identification of additional members of the activin/TGF-superfamily of

XX receptor proteins, and the coding sequences can be used for the

XX recombinant expression of the receptor proteins or functional fragments

XX of them. They may also be used to study the function and activity of

XX activin receptor polypeptides in cells and to identify agents which will

XX modulate activin receptor expression and activity for use in treating

XX conditions such as carcinogenesis, wound healing, disorders of the immune

XX or central nervous systems and especially the reproductive system (where

XX they may be used to control fertility in humans, domestic and commercial

XX animals).

XX Sequence 513 AA;

XX Query Match 99.7%; Score 2763; DB 20; Length 513;

XX Best Local Similarity 99.4%; Pred. No. 1.1e-270;

XX Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

DB 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

QY 61 FATWKNISGIEIVKQGCWLDINDYDRTDCVEKKDSPEVYFCCGEGNMCNEKESYFPEM 120

DB 61 FATWKNISGIEIVKQGCWLDINDYDRTDCIEKKDSPEVYFCCGEGNMCNEKESYFPEM 120

QY 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYVYRHHKWAYPPVLVPTQDGP 180

DB 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYVYRHHKWAYPPVLVPTQDGP 180

QY 181 PPSPLLLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKQSWQNEVEYVSLPG 240

DB 181 PPSPLLLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKQSWQNEVEYVSLPG 240

QY 241 MKHENILQFTGABKRGTSVDVDLWLITAFHEKGSLSDFLKANVYSWNQICHIAETMARGL 300

DB 241 MKHENILQFTGABKRGTSVDVDLWLITAFHEKGSLSDFLKANVYSWNQICHIAETMARGL 300

QY 301 AYLHEDIPLGDKGHPAISHRDIKSNVLLKNLTACTADFLGALKFPAKGSAGDTHGOV 360

DB 301 AYLHEDIPLGDKGHPAISHRDIKSNVLLKNLTACTADFLGALKFPAKGSAGDTHGOV 360

QY 361 GTRRYMAPEVLGAINFORDAFLRDMYAMGLVWELASRCTAAGDPVDEYMLPFEIEIG 420

DB 361 GTRRYMAPEVLGAINFORDAFLRDMYAMGLVWELASRCTAAGDPVDEYMLPFEIEIG 420

QY 421 QHPSLEDQVGVVHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480

DB 421 QHPSLEDQVGVVHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480

QY 481 QMORLNTIITTEDIVVTVMYTNVDPPKESL 513

DB 481 QMORLNTIITTEDIVVTVMYTNVDPPKESL 513

RESULT 6

AAB14797

ID AAB14797 standard; Protein: 513 AA.

XX AAB14797;

XX 11-DEC-2000 (first entry)

XX Mouse activin receptor.

XX TGF-beta superfamily protein receptor; activin receptor; mouse; MR-1;

XX Drosophila morphogen receptor; morphogen analogue identification;

XX OP-1; BMP-2; bone morphogenetic protein-2; in vivo binding; antagonist;

XX agonist; osteosarcoma; Paget's disease; tissue regeneration;

XX tissue repair; insecticide.

XX Mus sp.

XX US6093547-A.

XX 25-JUL-2000.

XX 02-JUN-1995; 95US-0459951.

XX 16-DEC-1994; 94US-0357533.

XX 07-JUN-1993; 93US-0073199.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Kuberampath T, Smart JE, Jin DF, Oppermann H.

XX WPI; 2000-531476/48.

XX Identifying morphogen analogs useful for designing morphogen agonists

XX and antagonists for therapeutic or diagnostic uses, comprises exposing

XX a candidate morphogen analog to a morphogen receptor-1 -

XX Example 1; Column 43-48; 31pp; English.

XX The invention relates to a method of identifying a morphogen analogue

XX and predicting whether it is capable of in vivo binding to a morphogen

XX receptor. The method comprises determining whether the candidate

XX morphogen analogue binds to the Drosophila morphogen receptor MR-1

XX (AAB14794), its allelic and species variants, or its isolated ligand

XX binding domain. The method is useful for identifying morphogen

XX analogues which may be used in therapeutic, diagnostic and

XX experimental research applications as morphogen agonists or

XX antagonists. Morphogen antagonists may be used to modulate uncontrolled

XX differentiated tissue growth such as malignant transformations in

XX osteosarcoma or Paget's disease, and as insecticides, which can

XX interfere with insect growth and tissue development. Morphogen agonists

XX are used where tissue morphogenesis is desired, e.g., in the

XX regeneration of damaged tissue resulting from mechanical or chemical

XX trauma, degenerative diseases, or tissue destruction. Sequences

XX AAB14795-B14798 represent receptors for TGF-beta superfamily proteins

XX which were used to design degenerate PCR primers (AAA7309-A7312). In an

XX exemplification of the invention, the primers were used to isolate a

XX probe (AAA7308) from Drosophila genomic DNA which was in turn used to

XX isolate cDNA encoding Drosophila MR-1 (AAA7307). The present sequence

XX represents a mouse activin receptor.

XX Sequence 513 AA;

XX Query Match 99.7%; Score 2763; DB 21; Length 513;

XX Best Local Similarity 99.4%; Pred. No. 1.1e-270;

XX Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

DB 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVCYGDGDKRRHC 60

QY 61 FATWKNISGIEIVKQGCWLDINDYDRTDCVEKKDSPEVYFCCGEGNMCNEKESYFPEM 120

DB 61 FATWKNISGIEIVKQGCWLDINDYDRTDCIEKKDSPEVYFCCGEGNMCNEKESYFPEM 120

QY 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYVYRHHKWAYPPVLVPTQDGP 180

DB 121 EVTQPTSNVTPKPPYNNILYSLVPLMLTAGIVICAFWYVYRHHKWAYPPVLVPTQDGP 180

QY 181 PPSPLLLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKQSWQNEVEYVSLPG 240

DB 181 PPSPLLLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKQSWQNEVEYVSLPG 240

QY 241 MKHENILQFTGABKRGTSVDVDLWLITAFHEKGSLSDFLKANVYSWNQICHIAETMARGL 300

DB 241 MKHENILQFTGABKRGTSVDVDLWLITAFHEKGSLSDFLKANVYSWNQICHIAETMARGL 300

Qy 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALKEAGKSGADTHGOV 360
Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALKEAGKSGADTHGOV 360
Qy 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420
Qy 421 QHPSLEDQMEVVVHKRRPVLRYWQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480
Db 421 QHPSLEDQMEVVVHKRRPVLRYWQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480
Qy 481 QMQRNLNIITTEDIVTVVMTVNTVDFPPKESL 513
Db 481 QMQRNLNIITTEDIVTVVMTVNTVDFPPKESL 513
RESULT 7
AAB47025
ID AAB47025 standard; Protein: 513 AA.
XX
AC AAB47025;
29-MAR-2001 (first entry)
Mouse activin receptor.
DE Mouse; human; rat; Xenopus; activin receptor; ligand binding domain;
KW transmembrane domain; receptor domain; serine kinase; TGF-beta;
KW transforming growth factor-beta; carcinogenesis; cancer;
KW wound healing.
XX Mus musculus.
OS
FH Key Location/Qualifiers
FT Peptide 1..19 /note= "Secretion signal peptide"
FT
XX
XX US6162896-A.
PN 19-DEC-2000.
PD
XX
PF 07-JUN-1995; 95US-0476123.
XX
XX 08-MAY-1992; 92US-0880220.
PR 10-MAY-1991; 91US-0698709.
PR 09-OCT-1991; 91US-0773229.
PR 02-SEP-1994; 94US-0300584.
XX
XX (SALK) SALK INST BIOLOGICAL STUDIES.
PA
XX Tsuchida K, Vale WW, Mathews LW;
DR WPI: 2001-090408/10.
DR N-PSDB; AAC85297.
XX
XX Novel vertebrate activin receptor having extracellular ligand binding
PT domain, transmembrane domain and intracellular serine/threonine kinase
PT domain is useful for diagnosing and treating e.g. carcinogenesis, wound
PT healing
XX
XX Claim 11; Column 27-30; 33pp; English.
XX
XX This sequence shows a mouse-derived activin receptor. The activin
CC receptors of the invention comprise three distinct domains: an
CC extracellular, ligand binding domain, a hydrophobic, transmembrane
CC domain and an intracellular, receptor domain having serine kinase-like
CC activity. These proteins have binding affinity for at least one
CC member of the activin/TGF-beta superfamily of polypeptide growth
CC factors. The activin receptor proteins of the invention can be
CC employed for a variety of therapeutic uses, e.g. to block receptors.
CC The presence of the soluble proteins will compete with functional
CC ligand for the receptor, preventing the formation of a functional

CC receptor-ligand complex, thereby blocking the normal regulatory
CC action of the complex. The receptor proteins are useful for the
CC diagnosis and therapeutic management of carcinogenesis, wound healing,
CC disorders of the immune, reproductive, or central nervous systems.
XX
SQ Sequence 513 AA;
Query Match 99.7%; Score 2763; DB 22; Length 513;
Best Local Similarity 99.4%; Pred. No. 1.1e-270;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGAACKLAFAVFLISCSGAIIIGRSETQCLFFNANWEKDRDNTQGVPCYGDKDRRHC 60
Db 1 MGAACKLAFAVFLISCSGAIIIGRSETQCLFFNANWEKDRDNTQGVPCYGDKDRRHC 60
Qy 61 FATWKNISGIEIVKQGCWLDDINCYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
Db 61 FATWKNISGIEIVKQGCWLDDINCYDRTDCIEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
Qy 121 EVTQPTSNPVTPKPPYYNILLYSLVPLMLIAGIVICAFWVYRHHKMAPVLPVPTQDPGP 180
Db 121 EVTQPTSNPVTPKPPYYNILLYSLVPLMLIAGIVICAFWVYRHHKMAPVLPVPTQDPGP 180
Qy 181 PPSPLLLGLKPLQLLEVKARGFCVVKQAQLLNEYVAVKIFPIQDKQSMONEYEYVSLPG 240
Db 181 PPSPLLLGLKPLQLLEVKARGFCVVKQAQLLNEYVAVKIFPIQDKQSMONEYEYVSLPG 240
Qy 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVWSNOLCHIAETMARGL 300
Db 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVWSNOLCHIAETMARGL 300
Qy 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALKEAGKSGADTHGOV 360
Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKVLLKNNLTACIADFGALALKEAGKSGADTHGOV 360
Qy 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWLWELASRCTAADGVPDEYMLPFEEIG 420
Qy 421 QHPSLEDQMEVVVHKRRPVLRYWQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480
Db 421 QHPSLEDQMEVVVHKRRPVLRYWQKHAGMAMLCETIEECWDHDAEALRSAGCVGERIT 480
Qy 481 QMQRNLNIITTEDIVTVVMTVNTVDFPPKESL 513
Db 481 QMQRNLNIITTEDIVTVVMTVNTVDFPPKESL 513
RESULT 8
AA014118
ID AA014118 standard; Protein: 513 AA.
XX
AC AA014118;
XX
XX 07-MAY-2002 (first entry)
XX
XX Protein of a mouse-derived activin receptor.
XX
XX Mouse; activin receptor; cloning; recombinant; TGF-beta; ligand-binding;
KW superfamily; trans-membrane; receptor domain; serine kinase; diagnosis;
KW therapeutic management; carcinogenesis; wound healing; protein therapy;
KW immune; reproductive; central nervous system; activin-dependent tumour;
KW brain neuron; abortion; livestock; twinning; probe; agonist; cytostatic;
KW wound healing; transplant organ rejection; vulnerability; immunosuppressive;
KW transforming growth factor-beta.
XX Mus sp.
XX
XX Location/Qualifiers
FH Key 1..10
FT Region /note= "Hydrophobic region"
FT Region 119..142
FT Region /note= "Membrane-spanning region"

CC activin-dependent tumours, for enhancing the survival of brain
CC neurons, for inducing abortion or twinning in livestock, for
CC stimulating wound healing, for suppression of growth of TGF-beta
CC sensitive tumours, for suppressing immune response, for promoting
CC liver regeneration and for stimulating some immune responses.
XX
SQ Sequence 513 AA;

Query Match 99.6%; Score 2758; DB 13; Length 513;
Best Local Similarity 99.2%; Pred. No. 3.6e-270;
Matches 509; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGAALKAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHC 60
Db 1 MGAALKAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHC 60

Qy 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNMCKNEKFSYFPEM 120
Db 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNMCKNEKFSYFPEM 120

Qy 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
Db 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180

Qy 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIFPTQDKOSWONEYEVS LPG 240
Db 181 PPPSLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIFPTQDKOSWONEYEVS LPG 240

Qy 241 MKHENILOFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVVSNOLCHIAETMARGL 300
Db 241 MKHENILOFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVVSNOLCHIAETMARGL 300

Qy 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACTADFGALKEAGKSDTHGQV 360
Db 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACTADFGALKEAGKSDTHGQV 360

Qy 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420

Qy 421 QHPSLEDQEVVHVHKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
Db 421 QHPSLEDQEVVHVHKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480

Qy 481 QMORLTNIITTEDIVVTVMVTNVDFFPKESSL 513
Db 481 HMORLTNIITTEDIVVTVMVTNVDFFPKESSL 513

RESULT 10
AAW26359
AAW26359 standard; Protein; 521 AA.

AC AAW26359;
XX
DT 02-DEC-1997 (first entry)
XX
DE Mouse activin receptor.
XX
KW Activin receptor; neuronal cell-specific receptor; mouse;
KW neurodegenerative disease; diagnosis.
OS Mus musculus.
FH
FT Key Location/Qualifiers
FT Misc-difference 1 /note= "residue 1 is (optionally protected) Met
FT /note= "or is replaced by hydrogen"
FT Peptide /note= "177..184
FT /note= "characteristic peptide of activin receptor
XX (Claim 1)"
PN EP771873-A2.

XX 07-MAY-1997.
XX
XX 25-OCT-1996; 96EP-0117125.
XX
XX 04-JUL-1996; 96JP-0174909.
XX 27-OCT-1995; 95JP-0280939.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Nakamura T, Shouji H, Sugino H;
XX
XX WPI; 1997-247415/23.
XX N-PSDB; AAT84517.
XX
XX Neuronal activin receptor protein and DNA - for use in drug
XX screening assays and diagnosis of neurodegenerative diseases
XX
XX Claim 4; Page 30-31; 40pp; English.
XX
XX This polypeptide sequence comprises a novel mouse activin receptor
XX whose expression is specific to the neuronal system and the whole
XX embryo. The sequence was deduced from a cDNA clone (AAT84517)
XX isolated from a mouse embryonal carcinoma cell line p19 whose
XX neuronal differentiation had been induced by retinoic acid. The
XX sequence includes an octapeptide (see AAW26360) that is highly
XX conserved in activin receptors, also being found in human and frog
XX sequences. The receptor, and DNA encoding it, can be used for
XX ligand determination, preparation of antibodies, construction of
XX recombinant receptor protein expression systems, development of
XX receptor binding assays and screening for pharmaceutical candidates,
XX drug design based on structurally similar ligand receptors.
XX construction of probes and primers (see AAT84518-19) for gene
XX detection (useful for the diagnosis of neurodegenerative diseases),
XX and for gene therapy.
XX
XX Sequence 521 AA;

Query Match 99.1%; Score 2744; DB 18; Length 521;
Best Local Similarity 97.9%; Pred. No. 9.7e-269;
Matches 509; Conservative 3; Mismatches 0; Indels 8; Gaps 1;

Qy 2 GAAKALAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHCF 61
Db 2 GAAKALAFVFLISCSGAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKRRHCF 61

Qy 62 ATWKNISGSIEIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNMCKNEKFSYFPEME 121
Db 62 ATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNMCKNEKFSYFPEME 121

Qy 122 VTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQ---- 176
Db 122 VTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQAFHI 181

Qy 177 ---DPGPPPPPLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIFPIQDKSQWNEY 233
Db 182 MIEDPGPPPPPLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIFPIQDKSQWNEY 241

Qy 234 EYVSLPGMKHENILOFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVVSNOLCHIA 293
Db 242 EYVSLPGMKHENILOFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVVSNOLCHIA 301

Qy 294 ETWARGLAYLHEDIPLGKDGHPKPAISHRDIKSNVLLKNNLTACTADFGALKEAGKSA 353
Db 302 ETWARGLAYLHEDIPLGKDGHPKPAISHRDIKSNVLLKNNLTACTADFGALKEAGKSA 361

Qy 354 GDTHGQVGTFRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAAGDPVDEYML 413
Db 362 GDTHGQVGTFRYMAPEVLEGAINFORDAFLRIDMYAGLVWLWELASRCTAAGDPVDEYML 421

Qy 414 PFEEIGQHPSLQEDQEVVHVHKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAG 473
Db 422 PFEEIGQHPSLQEDQEVVHVHKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAG 481

QY 474 CVGERITQMRLTNIITTDIVVTWTVNVDPPKESL 513
 DB 482 CVGERITQMRLTNIITTDIVVTWTVNVDPPKESL 521

RESULT 11

AAW93204
 ID AAW93204 standard; Protein; 510 AA.

AC AAW93204;

XX 27-MAY-1999 (first entry)

DE Xenopus activin receptor protein.

XX Activin receptor; activin/TGF-superfamily; receptor protein; function;
 XX activity; modulate; treatment; carcinogenesis; wound healing; fertility;
 XX immune system disorder; central nervous system disorder;
 KW reproductive system.

XX Xenopus sp.

XX US885794-A.

XX 23-MAR-1999.

XX 02-SEP-1994; 94US-0300584.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX Mathews LS, Vale WW;

XX WPI; 1999-228534/19.

XX N-PSDB; AAX22684.

XX Isolated nucleic acid molecules encoding vertebrate activin receptor
 XX polypeptides - useful as probes for detecting similar sequences and
 XX for investigating the function of the receptor in conditions such as
 XX carcinogenesis, wound healing and disorders of the immune, central
 XX nervous and reproductive systems

XX Claim 29; Column 33-36; 28pp; English.

XX This sequence represents a Xenopus sp. activin receptor polypeptide.
 XX The nucleic acid molecules of the invention are useful as probes for the
 XX identification of additional members of the activin/TGF-superfamily of
 XX receptor proteins, and the coding sequences can be used for the
 XX recombinant expression of the receptor proteins or functional fragments
 XX of them. They may also be used to study the function and activity of
 XX activin receptor polypeptides in cells and to identify agents which will
 XX modulate activin receptor expression and activity for use in treating
 XX conditions such as carcinogenesis, wound healing, disorders of the immune
 XX or central nervous systems and especially the reproductive system (where
 XX they may be used to control fertility in humans, domestic and commercial
 XX animals).

XX Sequence 510 AA;

Query Match 71.2%; Score 1971.5; DB 20; Length 510;
 Best Local Similarity 67.9%; Pred. No. 1.7e-190;
 Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAANKAFAPVLISCSGAILGRSETOECLFFNANWEKORTNQTGVEPCYGDKRRHC 60

DB 1 MGASVALTFLLLATFRAGSGHDEVTRECIYYNANWELEKTNOSGVESCEGEKRLHC 60

QY 61 FATWKNISGISIEIVKQGCWLDIDINCYDRTDCVEKKDSPEVVFCCCEGNCMKNFVSFPEM 120

DB 61 YASWRNNSGFEIVKKGWLDDENCYDROECIAKENPQVFCCCBGNYCNKFKTHLPEV 120
 QY 121 EVTQPTSNPTKPPYYNILLYSILVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDQGP 180
 DB 121 ETDFDKQ---PSASVLNLIYISLLPIVGLSMAILAFWYRHHKPPYGHVEI-NEDFGL 176
 QY 181 PPSPLGLKPLQLLEVKARGFCVWKAQLNNEYVAVKIFPIQDKOSWONEYEYSLPG 240
 DB 177 PPSPLVGLKPLQLLEIKARGFCVWKAQLNNEYVAVKIFPIQDKOSWONEYEYSLPG 236
 QY 241 MKHENILOFTCAKRGTSVDVLDLWLTAFHEKGSLSDELKANVYSNOLCHIAETMARGL 300
 DB 237 MKHENLEFIAAARGSNLEMLWLTAFHDKGSLDYILKGNLVSNELCHITETMARGL 296
 QY 301 AYLEDIPGLK-DGHKPAISHRIDIKSKNVLKNNLTACIADFGALAKFAGKSAGSDTHGQ 359
 DB 297 AYLEDVPRCKGECHKPAIAHRDFKSKNVLRLNDLTAILADFGAVRFEPPGKPGDTHGQ 356
 QY 360 VGTTRYMAPEVLEGAINFQDAFLRDMYAMGLVIMELASRCTAADGPDVEYMLPEEEI 419
 DB 357 VGTTRYMAPEVLEGAINFQDSFLRDMYAMGLVIMELASRCTAADGPDVEYMLPEEEI 416
 QY 420 GQHPSEDMQEVVVKKRPVLRDYMOKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
 DB 417 GQHPSEDLQEVVVKKRPVLRDYMOKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 476
 QY 480 TOMORLNTIITDITVIVTWTNVDPPKESL 513
 DB 477 SQIRKSVNGTSDCLVSVITSVTNVDLPPKESI 510

RESULT 12

AAW47026
 ID AAW47026 standard; Protein; 510 AA.

XX AAW47026;

XX 29-MAR-2001 (first entry)

XX Xenopus activin receptor.

XX Mouse; human; rat; Xenopus; activin receptor; ligand binding domain;
 KW transmembrane domain; receptor domain; serine kinase; TGF-beta;
 KW transforming growth factor-beta; carcinogenesis; cancer;
 KW wound healing.

XX Xenopus laevis.

XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Secretion signal peptide"

XX US6162896-A.

XX 19-DEC-2000.

XX 07-JUN-1995; 95US-0476123.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Tsuchida K, Vale WW, Mathews LW;

XX WPI; 2001-090408/10.

XX N-PSDB; AAC85298.

XX Novel vertebrate activin receptor having extracellular ligand binding
 PT domain, transmembrane domain and intracellular serine/threonine kinase

PT domain is useful for diagnosing and treating e.g. carcinogenesis, wound
 PT healing

PS Claim 11; Column 33-36; 33pp; English.

XX This sequence shows a frog-derived activin receptor. The activin
 CC receptors of the invention comprise three distinct domains: an
 CC extracellular, ligand binding domain, a hydrophobic, transmembrane
 CC domain and an intracellular, receptor domain having serine kinase-like
 CC activity. These proteins have binding affinity for at least one
 CC member of the activin/TGF-beta superfamily of polypeptide growth
 CC factors. The activin receptor proteins of the invention can be
 CC employed for a variety of therapeutic uses, e.g. to block receptors.
 CC The presence of the soluble proteins will compete with functional
 CC ligand for the receptor, preventing the formation of a functional
 CC receptor-ligand complex, thereby blocking the normal regulatory
 CC action of the complex. The receptor proteins are useful for the
 CC diagnosis and therapeutic management of carcinogenesis, wound healing,
 CC disorders of the immune, reproductive, or central nervous systems.

XX Sequence 510 AA;

Query Match 71.2%; Score 1971.5; DB 22; Length 510;
 Best Local Similarity 67.9%; Pred. No. 1.7e-190;
 Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAARAKLAFVFLISCSGAILGRSETQCLFFNANNEKDRNTOTGVEPCYGDKRRHC 60
 DB 1 MGASVALFTLLLATFRAGSGHDEVETRECIYNNANNELEKTNQSGVESCEGEKDRKLC 60
 QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTDCEVKKDSPEVYFCCCEGNCNKFSPFPM 120
 DB 61 YASWRNNSGFIELYKKGWLDIDNCYDRTDCEVKKDSPEVYFCCCEGNCNKFTHLPEV 120
 QY 121 EYQTSNPVTPKPPYNYLISVPLMLIAGIVICAFWYRHHKMAPPPVLPVTPDGP 180
 DB 121 EYFDPKPPQ---PSASVNLILYSLPIVGLSMAILLAFWYRHHKMAPPPVLPVTPDGP 176
 QY 181 PPSPLGLKPLQLLEKARFGVCWKAQLLNEYVAVKIPIDQKOSQWNEYEVYSLPG 240
 DB 177 PPSPLVGLKPLQLLEKARFGVCWKAQLLNEYVAVKIPVQDKSQWCEKEFTTTPG 236
 QY 241 MKHENILQFAGKRGTSVDVLDLWITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
 DB 237 MKHENLEFIAAEKRGSNLEMLWITAFHDKGSITDYLKGNLYVSNELCHITETMARGL 296
 QY 301 AYLHEDIPGLK-DGHPKPAISHRDIKSKNVLKNNLTACIADFGALKPEAGKSGADTHGQ 359
 DB 297 AYLHEDVPRCKGEGHKAHAHRDFKSNVLLKNDUTAILADFGLAVERPKPGDTHGQ 356
 QY 360 VGTTRYMAPEVLEGAINFQDAFLRIDMYAMGLVLWELASRCTAAGDPVDEYMLPFEEI 419
 DB 357 VGTTRYMAPEVLEGAINFQDSFLRIDMYAMGLVLWELVSRCTAAGDPVDEYMLPFEEI 416
 QY 420 GHPSLEDQEVVVKHKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
 DB 417 GHPSLEDLQEVVVKHKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 476
 QY 480 TQWORTNLITTEDIVTVVTNVDFFPKESL 513
 DB 477 SQIRKSVNGTSDCLVSIIVTNTVDLPKESSI 510

RESULT 13

AA014119
 ID AA014119 standard; Protein; 510 AA.

XX AC AA014119;

XX DT 07-MAY-2002 (first entry)

XX DE Protein of a Xenopus-derived activin receptor.

XX

KW Activin receptor; cloning; recombinant; TGF-beta; ligand-binding;
 KW superfamily; trans-membrane; receptor domain; serine kinase; diagnosis;
 KW therapeutic management; carcinogenesis; wound healing; protein therapy;
 KW immune; reproductive; central nervous system; activin-dependent tumour;
 KW brain neuron; abortion; livestock; twinning; probe; agonist; cytostatic;
 KW wound healing; transplant organ rejection; vulnery; immunosuppressive;
 KW transforming growth factor-beta; amphibian.

XX Xenopus sp.

XX US2001039036-A1.

XX 08-NOV-2001.

XX 19-DEC-2000; 2000US-0742684.

XX 07-JUN-1995; 95US-0476123.

XX 08-MAY-1992; 92US-0880220.

XX 10-MAY-1991; 91US-0698709.

XX 09-OCT-1991; 91US-0773229.

XX 02-SEP-1994; 94US-0300584.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Mathews LS, Vale WW, Tsuchida K;

XX WPI; 2002-040721/05.

XX N-PSDB; AAK98721.

XX New receptor proteins having an extracellular ligand-binding domain, a
 PT hydrophobic trans-membrane domain, and an intracellular receptor
 PT domain, useful for diagnosing or treating carcinogenesis, wound healing
 PT or immune disorders

XX Claim 5; Page 19-20; 33pp; English.

XX This sequence represents the protein of a Xenopus-derived activin
 CC receptor. The invention relates to cloning and recombinant production of
 CC receptor(s) of the activin/TGF-beta (transforming growth factor-beta)
 CC superfamily. The invention has identified and characterised members of a
 CC new superfamily of receptor proteins which comprise three distinct
 CC domains: an extracellular, ligand-binding domain, a hydrophobic, trans-
 CC membrane domain, and an intracellular, receptor domain having serine
 CC kinase-like activity. The receptor proteins and antibodies to these
 CC proteins are useful in the diagnosis and therapeutic management of
 CC carcinogenesis, wound healing, disorders of the immune, reproductive, or
 CC central nervous systems. The receptor proteins of the invention can be
 CC used in protein therapy. These may further be used to diagnose or treat
 CC activin-dependent tumours, enhance the survival of brain neurons, induce
 CC abortion in livestock and other domesticated animals, and induce twinning
 CC in livestock and other domesticated animals. The DNAs are useful as
 CC probes for identifying additional members of the superfamily of receptor
 CC proteins, and as coding sequences which can be used for the recombinant
 CC expression of the receptor proteins. Agonists for TGF-beta specific
 CC receptors can be used to stimulate wound healing, to suppress growth of
 CC TGF-beta sensitive tumours, or to suppress immune response (thus prevent
 CC rejection of transplant organ). The receptor proteins of the invention
 CC have cytostatic, vulnery, and immunosuppressive activity.

XX Sequence 510 AA;

Query Match 71.2%; Score 1971.5; DB 23; Length 510;
 Best Local Similarity 67.9%; Pred. No. 1.7e-190;
 Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAARAKLAFVFLISCSGAILGRSETQCLFFNANNEKDRNTOTGVEPCYGDKRRHC 60
 DB 1 MGASVALFTLLLATFRAGSGHDEVETRECIYNNANNELEKTNQSGVESCEGEKDRKLC 60

QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTDCEVKKDSPEVYFCCCEGNCNKFSPFPM 120
 DB 61 YASWRNNSGFIELYKKGWLDIDNCYDRTDCEVKKDSPEVYFCCCEGNCNKFTHLPEV 120

QY 121 EVTQTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWVYRHHKMAYPVLPVPTDQGP 180
 Db 121 ETEDPKPQ---PSASVLNLLIYSLLPVGLSMALLAFWYRHHKPPYGHVEI-NEDPGL 176
 QY 181 PPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYVYSLPG 240
 Db 177 PPSPLVGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWCEKEIFTTPG 236
 QY 241 MKHENILQFAGKRGTSVDVDLWLITAFHEKGSLSDFLKVANVSNOLCHIAETMARGL 300
 Db 237 MKHENLEFIAEAKRGSNLEMLWLTAFHDKGSLTDYLGKLVSNWELCHITETMARGL 296
 QY 301 AYLEDIPGLK-DGHKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGQ 359
 Db 297 AYLEDVPRCKGEGHKAIAHRDFKSNVLLRNDLTAILADFGLAVERFEPCKPGDTHGQ 356
 QY 360 VGTTRYMAPEVLEGAINFQDARFLRDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEI 419
 Db 357 VGTTRYMAPEVLEGAINFQDARFLRDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEI 416
 QY 420 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECWHDHAEARLSAGCVGERI 479
 Db 417 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECWHDHAEARLSAGCVGERI 476
 QY 480 TOMORLNTIITTEDIVVTVMVTVNDFPPKESL 513
 Db 477 SQIRKSVNGTSDCLVSIVTSVTNVDLPKKESSI 510
 RESULT 15
 AAR29582
 ID AAR29582 standard; Protein; 510 AA.
 AC AAR29582;
 DT 19-APR-1993 (first entry)
 DE Xenopus activin receptor.
 KW Activin receptor; mouse; Xenopus; human; extracellular; ligand binding;
 KW hydrophobic; trans-membrane; intracellular; receptor; domain;
 KW serine kinase-like; activity; probe; superfamily; secretion signal;
 KW golgi membrane; diagnosis; treatment; activin-dependent tumour; brain;
 KW neuron; abortion; twinning; wound healing; TGF-beta; immune response;
 KW liver regeneration.
 XS Xenopus laevis.
 XX WO9220793-A.
 XX 26-NOV-1992.
 XX 08-MAY-1992; 92WO-US03825.
 PR 10-MAY-1991; 91US-0698709.
 PR 09-OCT-1991; 91US-0773229.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA Mathews LS, Vale WW;
 XX WPI: 1992-415771/50.
 DR N-PSDB; AAQ31911.
 XX New member of activin-transforming growth factor beta
 PT super-family - for diagnosis and treatment of cancer and
 PT disorders of the immune, reproductive or central nervous system
 XX Disclosure; Page 47-49; 68pp; English.
 PS The sequences given in AAR29581-83 represent activin receptors from
 CC mouse, Xenopus and human respectively. Each of these proteins
 CC comprise three distinct domains; an extracellular, ligand binding

CC domain, a hydrophobic, trans-membrane domain and an intracellular,
 CC receptor domain having serine kinase-like activity. The DNA sequences
 CC encoding these proteins can be used as probes for the identification
 CC of additional members of this superfamily of receptor molecules. The
 CC proteins may further comprise a second hydrophobic domain at the amino
 CC terminal which comprises a secretion signal sequence which promotes
 CC the intracellular transport of the initially expressed receptor
 CC protein across the golgi membrane. These receptor proteins can be
 CC used to develop agents for the diagnosis and/or treatment of eg.
 CC activin-dependent tumours, for enhancing the survival of brain
 CC neurons, for inducing abortion or twinning in livestock, for
 CC stimulating wound healing, for suppression of growth of TGF-beta
 CC sensitive tumours, for suppressing immune response, for promoting
 CC liver regeneration and for stimulating some immune responses.
 XX

SQ Sequence 510 AA;

Query Match 71.1%; Score 1968.5; DB 13; Length 510;
 Best Local Similarity 67.7%; Pred. No. 3.5e-190;
 Matches 348; Conservative 86; Mismatches 75; Indels 5; Gaps 3;
 QY 1 MGAARKLAFVAVLISCSGAILGRSETQECLEFFANWKEKRTNQTGVEPCYGDKKRRHC 60
 Db 1 MGASVALFTFLLLATFRAGSGHDEVETRECIYANWNELEKTNQSGVSCGEKDKRLHC 60
 QY 61 FATWKNISGSEIVKQGCWLDIDINCYDRTDCVEKKDPEVYFCCEGNCMEKESYEPFM 120
 Db 61 YASWNNSGFTELKKGKGLDIDFNCYDQECIAKEENQVFFCCGECYCNKRFTHLPEV 120
 QY 121 EVTQTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWVYRHHKMAYPVLPVPTDQGP 180
 Db 121 ETEDPKPQ---PSASVLNLLIYSLLPVGLSMALLAFWYRHHKPPYGHVEI-NEDPGL 176
 QY 181 PPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYVYSLPG 240
 Db 177 PPSPLVGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKOSQWCEKEIFTTPG 236
 QY 241 MKHENILQFAGKRGTSVDVDLWLITAFHEKGSLSDFLKVANVSNOLCHIAETMARGL 300
 Db 237 MKHENLEFIAEAKRGSNLEMLWLTAFHDKGSLTDYLGKLVSNWELCHITETMARGL 296
 QY 301 AYLEDIPGLK-DGHKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGQ 359
 Db 297 AYLEDVPRCKGEGHKAIAHRDFKSNVLLRNDLTAILADFGLAVERFEPCKPGDTHGQ 356
 QY 360 VGTTRYMAPEVLEGAINFQDARFLRDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEI 419
 Db 357 VGTTRYMAPEVLEGAINFQDARFLRDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEI 416
 QY 420 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECWHDHAEARLSAGCVGERI 479
 Db 417 GOHPSLEDQEVVYVHKRPVLDYVWQKHAGMAMLCETIECWHDHAEARLSAGCVGERI 476
 QY 480 TOMORLNTIITTEDIVVTVMVTVNDFPPKESL 513
 Db 477 SQIRKSVNGTSDCLVSIVTSVTNVDLPKKESSI 510

RESULT 15
 AAR29582
 ID AAR29582 standard; Protein; 512 AA.
 XX AAR29582;
 XX 16-FEB-1999 (first entry)
 DT Mouse ActRIIB2 receptor protein.
 DE Bone morphogenetic protein; BMP; BMP receptor kinase; ActRIIB receptor;
 KW BSK; receptor ligand; drug.
 XX Mus sp.
 OS

Tue May 13 17:51:38 2003

QY 487 NIITTEDIVTVVTVMTNVDFFPKESSL 513
Db 486 NGTTSCLVSLVTSVTNVDLLPKESSI 512

Search completed: May 10, 2003, 17:58:58
Job time : 80 secs

PN W09852038-A1.
XX 19-NOV-1998.
XX 13-MAY-1998; 98WO-US09519.
XX 16-MAY-1997; 97US-0046768.
XX (PROC) PROCTER & GAMBLE CO.
XX Rosenbaum JS;
XX WPI; 1999-009930/01.
XX N-PSDB; AAV71967.
XX
XX Screening method using bone morphogenetic protein receptor complex -
XX which binds to potential drugs, and ActRIIB receptor used in the
XX complex, also host cells transfected with DNA encoding the complex
XX
XX Claim 1; Pages 55-57; 110pp; English.
XX
XX This represents a mouse ActRIIB2 receptor protein. This can be used in
XX the method of the invention of determining whether a compound can bind to
XX a bone morphogenetic protein (BMP) receptor kinase protein complex. The
XX method comprises allowing a compound in a sample to bind to the complex,
XX where the complex is comprised of (i) a BMP; (ii) a BMP receptor kinase
XX protein (BRK); (iii) an ActRIIB receptor. The method can be used to
XX determine the concentration of a BMP receptor ligand in a sample by
XX comparing the binding to a standard curve prepared with known
XX concentrations of BMP ligand. The method can also be used to determine
XX whether a test compound produces a signal on binding to a BMP receptor
XX protein complex. The method is useful for determining whether a ligand,
XX such as a known or putative drug, can bind to and/or activate the
XX receptors.
XX
XX Sequence 512 AA;
SQ
Query Match 69.9%; Score 1935; DB 20; Length 512;
Best Local Similarity 67.3%; Pred. No. 8.6e-187;
Matches 341; Conservative 88; Mismatches 76; Indels 2; Gaps 2;
QY 8 AFAYFLISCSGAILGRSETOELFFNANWEKDRNTGVEPCYGDKDRRHCFATWKNI 67
Db 7 ALALWGLSCAGSGEAEARECIYYNANWELERTNQSLGREGCEQDKRLHCYASWRNS 66
QY 68 SGTIEIVKQGCWLDINCYDRTDCVERKKDSEPVYFCCEGNCMCNKFSPPEMEVTOPTS 127
Db 67 SGTIELVKKGCWLDNFCYDRQECVATEENPQVYFCCEGNCNCFERFTHLPEPGPEVY 126
QY 128 NPVTPKPPYYNLLYSLVPLMLIAGIVICAFWYVYRHMKMAYPPVLVPTQDPGPPPPSPLL 187
Db 127 EPPPTAPTLLTAVLAYSLPIGGLSLIVLLAFWYVYRHMKMAYPPVYVYVYVYVYVYVYVYVY 185
QY 188 GLKPLQLLEVKARGFCGVKQAQLLNEVAVKIPFIQDKSQWQNEVYVYVYVYVYVYVYVYVY 247
Db 186 GLKPLQLLEIKARGFCGVKQAQLMNDVAVKIPFIQDKSQWQNEVYVYVYVYVYVYVYVYVY 245
QY 248 QFIGAERKRTSVYDVLWLITAFHEKGSLSDFLKANVYVYVYVYVYVYVYVYVYVYVYVY 307
Db 246 QFIAAEKRGSLNLEVLWLTAFHDKGSLTDYLGKNIITWNLCHVAETMSRGLSYLHEDV 305
QY 308 PGLK-DGHHKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGQVGTTRYM 366
Db 306 PWCGRGEGHKPSIAHRDFKSNVLLKSDLTAVLADFGLAVERPEGKPGDTHGQVGTTRYM 365
QY 367 APEVLEGAINFORDAFLIDYVAMGLVWELASRCTAADGPVDEYMLPFEEIGOHPSLE 426
Db 366 APEVLEGAINFORDAFLIDYVAMGLVWELVSRCKAADGPVDEYMLPFEEIGOHPSLE 425
QY 427 DMQEVVHHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMORLT 486
Db 426 ELQEVVHHKKRPTIKDHLWHPGLAQLCVTEECWDHDAEARLSAGCVGERVSLIRRSV 485

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 17:57:45 ; Search time 24 seconds
(without alignments)
1967.050 Million cell updates/sec

Title: US-09-742-684A-16
Perfect score: 2770
Sequence: 1 MGAANKLAFVFLISCSGA.....IVTVMTVINVDPPKESL 513

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2763	99.7	513	10	US-09-742-684-2
2	1971.5	71.2	510	10	US-09-742-684-4
3	1150.5	41.5	516	9	US-10-108-605-79
4	1147.5	41.4	516	9	US-10-108-605-157
5	775.5	28.0	567	10	US-09-878-905-11
6	775.5	28.0	592	9	US-09-917-788-5
7	775.5	28.0	1038	10	US-09-908-500A-2
8	681	24.6	1080	10	US-09-904-380-2
9	674	24.3	532	9	US-09-982-543A-6
10	674	24.3	532	9	US-10-153-217-2
11	674	24.3	532	10	US-09-903-068-6
12	669	24.2	532	10	US-09-903-068-14
13	664	24.0	532	10	US-09-874-628-2
14	653.5	23.6	502	9	US-10-044-716-14
15	653.5	23.6	502	10	US-09-874-628-4
16	647.5	23.4	502	9	US-09-982-543A-8
17	647.5	23.4	502	10	US-09-903-068-18
18	643.5	23.2	493	9	US-09-069-228-2
19	637.5	23.0	493	10	US-09-742-684-12

20	624	22.5	503	10	US-09-903-068-10	Sequence 10, Appl
21	622.5	22.5	503	10	US-09-874-628-10	Sequence 10, Appl
22	615.5	22.2	505	10	US-09-903-068-8	Sequence 8, Appl
23	613.5	22.1	505	10	US-09-771-161A-200	Sequence 200, App
24	606.5	21.9	505	10	US-09-903-068-16	Sequence 16, Appl
25	606.5	21.9	505	10	US-09-874-628-8	Sequence 8, Appl
26	587.5	21.2	509	9	US-09-982-543A-4	Sequence 4, Appl
27	587.5	21.2	509	9	US-10-005-228-2	Sequence 2, Appl
28	587.5	21.2	509	10	US-09-903-068-4	Sequence 4, Appl
29	576	20.8	503	9	US-09-982-543A-2	Sequence 2, Appl
30	576	20.8	503	9	US-10-005-228-4	Sequence 4, Appl
31	576	20.8	503	10	US-09-903-068-2	Sequence 2, Appl
32	575.5	20.8	509	10	US-09-874-628-6	Sequence 6, Appl
33	549	19.8	502	10	US-09-903-068-12	Sequence 12, Appl
34	346	12.5	139	10	US-09-205-658-20	Sequence 20, Appl
35	346	12.5	139	10	US-09-844-353A-20	Sequence 20, Appl
36	316	11.4	198	10	US-09-925-302-500	Sequence 500, App
37	291.5	10.5	518	10	US-09-771-161A-231	Sequence 231, App
38	282.5	10.2	497	10	US-09-862-027-8	Sequence 8, Appl
39	280	10.1	478	9	US-09-866-050A-512	Sequence 512, App
40	274	9.9	460	9	US-10-001-254-16	Sequence 16, Appl
41	274	9.9	460	9	US-09-759-595-1	Sequence 1, Appl
42	270.5	9.8	460	9	US-10-001-254-28	Sequence 28, Appl
43	268	9.7	459	9	US-09-759-595-3	Sequence 3, Appl
44	265.5	9.6	825	9	US-10-101-464A-922	Sequence 922, App
45	262	9.5	277	9	US-10-172-088-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-742-684-2
; Sequence 2, Application US/09742684
; Patent No. US20010039036A1
; GENERAL INFORMATION:
; APPLICANT: Mathews, Lawrence S.
; Tsuchida, Kunihiko
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09742,684
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,123
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/300,584
; FILING DATE: 02-SEP-1994
; APPLICATION NUMBER: US 07/880,220
; FILING DATE: 08-MAY-1992
; APPLICATION NUMBER: US 07/773,229
; FILING DATE: 09-OCT-1991
; APPLICATION NUMBER: US 07/698,709
; FILING DATE: 10-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9927

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-742-684-2

Query Match          99.7%; Score 2763; DB 10; Length 513;
Best Local Similarity 99.4%; Pred. No. 7.9e-218;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRDTNQTGVPCYGDKRRHC 60
DB 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRDTNQTGVPCYGDKRRHC 60

QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTDCVEKKDSEVYFCCCEGNCNEKESYFPEM 120
DB 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTDCIEKKDSEVYFCCCEGNCNEKESYFPEM 120

QY 121 EVTQPTSNPVTKPPYYNILLISVPLMLIAGIVICAFWYRHHKMAYPVLPVTPDGP 180
DB 121 EVTQPTSNPVTKPPYYNILLISVPLMLIAGIVICAFWYRHHKMAYPVLPVTPDGP 180

QY 181 PPPSPLGLKPLQLLEVKARGFCVWKQAQLLNEYVAVKIFPTQDKOSWQNEVEYSLPG 240
DB 181 PPPSPLGLKPLQLLEVKARGFCVWKQAQLLNEYVAVKIFPTQDKOSWQNEVEYSLPG 240

QY 241 MKHENILQFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVYVSNOLCHIAETMARGL 300
DB 241 MKHENILQFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVYVSNOLCHIAETMARGL 300

QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQV 360

QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWELASRCTAADGVDVDEYVLPFEEIG 420
DB 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWELASRCTAADGVDVDEYVLPFEEIG 420

QY 421 QHPSEDMEQVYVHKKRPVLDYQKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 480
DB 421 QHPSEDMEQVYVHKKRPVLDYQKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 480

QY 481 QMRQLNTIITTEDIVVTVMVTNVDFFPKESSL 513
DB 481 QMRQLNTIITTEDIVVTVMVTNVDFFPKESSL 513

RESULT 2
US-09-742-684-4
; Sequence 4, Application US/09742684
; Patent No. US20010039036A1
; GENERAL INFORMATION:
; APPLICANT: Mathews, Lawrence S.
; Tsuchida, Kunihito
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
; NUMBER OF SEQUENCE: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/742,684
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,123
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/300,584
; FILING DATE: 02-SEP-1994
; APPLICATION NUMBER: US 07/880,220
; FILING DATE: 08-MAY-1992
; APPLICATION NUMBER: US 07/773,229
; FILING DATE: 09-OCT-1991
; APPLICATION NUMBER: US 07/698,709
; FILING DATE: 10-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 510 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-742-684-4

Query Match          71.2%; Score 1971.5; DB 10; Length 510;
Best Local Similarity 67.9%; Pred. No. 4.2e-153;
Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAALKAFVFLISCSGAILGRSETQCLFFNANWEKDRDTNQTGVPCYGDKRRHC 60
DB 1 MGAASVALTEILLIATFRAGSGHDEVETRECIYVNNANWELEKTNQSGVESCEGEKRLHC 60

QY 61 FATWKNISGSIEIVKQGCWLDIDNCYDRTDCVEKKDSEVYFCCCEGNCNEKESYFPEM 120
DB 61 YASWRNNSGFIELVKKGCWLDIDNCYDROECIAEENPOVFCECCGNYCNKKFTHLPEV 120

QY 121 EVTQPTSNPVTKPPYYNILLISVPLMLIAGIVICAFWYRHHKMAYPVLPVTPDGP 180
DB 121 ETEFDPKQ---PSASVNLIIYSLDPIVGLSMAILAFWYRHHKPPYGHVEI-NEDPGL 176

QY 181 PPPSPLGLKPLQLLEVKARGFCVWKQAQLLNEYVAVKIFPTQDKOSWQNEVEYSLPG 240
DB 177 PPPSPLVGLKPLQLLEIKARGFCVWKARLLNEYVAVKIFPVQDKQSQCEKEIFTTPG 236

QY 241 MKHENILQFICAEKRGTSVDVLDLITAFHEKGSLSDFLKVYVSNOLCHIAETMARGL 300
DB 237 MKHENLEFIAAEKRGSLNEMELWLITAFHDGSLTDYLLKGLVSNWELCHITETMARGL 296

QY 301 AYLEDIPGLK-DGHPKPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 359
DB 297 AYLEDVPRCKGEGHPKPAIAHRDFKSNVLLRNDLTAILADFGLAVERFEPGPGDTHGQ 356

QY 360 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWELASRCTAADGVDVDEYVLPFEEI 419
DB 357 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWELASRCTAADGVDVDEYVLPFEEI 416

QY 420 QHPSEDMEQVYVHKKRPVLDYQKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERI 479
DB 417 QHPSEDMEQVYVHKKRPVLDYQKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERI 476

QY 480 QMRQLNTIITTEDIVVTVMVTNVDFFPKESSL 513
DB 477 SQIRKSVNGTTSCLVSIYVTSVTNVDLPKESSI 510
```

RESULT 3

US-10-108-605-79

; Sequence 79, Application US/10108605

; Patent No. US20020160934A1

; GENERAL INFORMATION:

; APPLICANT: Broadus, Julie

; APPLICANT: Stam, Lynn

; APPLICANT: Bachmann, Jane

; APPLICANT: Kamdar, Kim

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE

; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

; FILE REFERENCE: 31133B

; CURRENT APPLICATION NUMBER: US/10/108,605

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: US 09/761,142

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/176,418

; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 361

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 79

; LENGTH: 516

; TYPE: PRF

; ORGANISM: Drosophila melanogaster

US-10-108-605-79

Query Match 41.5%; Score 1150.5; DB 9; Length 516;

Best Local Similarity 47.2%; Pred. No. 66; 86;

Matches 249; Conservative 83; Mismatches 152; Indels 43; Gaps 17;

QY 5 AKLAFVAVLISCGSAILGRSETQCLFFNANWEK--DRTNQ--TGVEPCYGDKKRRHC 60

Db 11 AQLTVCCLLIGHGSLPGSHGIECEHFD---EKMNCNTQOCETRIECHKMEADKFPSC 67

QY 61 FATW--KNISGSIEIVKQCWLDINCVDYDRCVEKKDSPE--VYFCCEGNCMEKFSY 116

Db 68 YVLSVNETGILRIKMKGCFTDMHEC--NOTECVTSAPROGNIHFCCCKGSRCSNQY 126

QY 117 FPE-----MEVYQPTSNPVPKPPYNYLLSLVPLMLIAGIVICAFVYVHHKMA 167

Db 127 IKSTTEATQVPKEKTQGSNLIY---IYIGTSVFSV--LMVIVGM---GLLLYRRRQKA 178

QY 168 YPVLVPTQDPPPPSPLLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKQ 227

Db 179 HFNE-IPTHEAEITNSPPLSNRPQLLEQKASGRFGDVQAKLNQDVAVKIFRMQKE 237

QY 228 SHQNEYEYVSLPGMKHENILQFIGAERKGTSDV--VDMLITAFHEKGSLSDFLKANYVSW 286

Db 238 SWTTEHDYKLPFRMRHPNILEFLGVEKH---MDKPEYWLSTYQHNGSLCDYLKSHTSW 294

QY 287 NOLCHIAETMARGLAYLHEDIPGLK--DGHKPAISHRDITKSNVLLKNNLTACIADFG 345

Db 295 PELCIAESMANGLAHLHEEIPASKTDGLKPSIAHRDFKSNVLLKSDLTACIADFG 354

QY 346 KFEAGKSAGDTHGOVGTTRYMAPEVELEGAINFQDAFLRIDMYAMGLVWELASRCTA 405

Db 355 IFQPKPCGDTHGOVGTTRYMAPEVELEGAINFQDAFLRIDMYAMGLVWELASRCTA 413

QY 406 GPVDEYMLPFEEIQHPSLEDMQEVVYVHKRPVLRDYWKHAGMAMLCETIEECWDHD 465

Db 414 GPVGEFQLPFAELGLRSLDEVOESVYMKLRPRLNLSWRAHPLGVLNFCDTMEECWD 473

QY 466 AEARLSACVGERITQMRITNIITTEDIVTVMTNVDFPPPKSS 512

Db 474 AEARLSSVCYMERFAQLNKYPS-----TQLLIKHTNID-DAKEST 513

RESULT 4

US-10-108-605-157

; Sequence 157, Application US/10108605

; Patent No. US20020160934A1

; GENERAL INFORMATION:

; APPLICANT: Broadus, Julie

; APPLICANT: Stam, Lynn

; APPLICANT: Bachmann, Jane

; APPLICANT: Kamdar, Kim

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE

; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

; FILE REFERENCE: 31133B

; CURRENT APPLICATION NUMBER: US/10/108,605

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: US 09/761,142

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/176,418

; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 361

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 157

; LENGTH: 516

; TYPE: PRF

; ORGANISM: Drosophila melanogaster

US-10-108-605-157

Query Match 41.4%; Score 1147.5; DB 9; Length 516;

Best Local Similarity 47.8%; Pred. No. 11e-85;

Matches 251; Conservative 83; Mismatches 144; Indels 47; Gaps 19;

QY 11 VFLISC---SSGAIL-CRSETQCLFFNANWEK--DRTNQ--TGVEPCYGDKKRRHCFA 62

Db 13 VTLVCCLLIGHGSLPGSHGIECEHFD---EKMNCNTQOCETRIECHKMEADKFPSCYV 69

QY 63 TW--KNISGSIEIVKQCWLDINCVDYDRCVEKKDSPE--VYFCCEGNCMEKFSYFP 118

Db 70 LWSVNETGILRIKMKGCFTDMHEC--NOTECVTSAPROGNIHFCCCKGSRCSNQYIK 128

QY 119 E-----MEVYQPTSNPVPKPPYNYLLSLVPLMLIAGIVICAFVYVHHKMAYP 169

Db 129 STTEATQVPKEKTQGSNLIY---IYIGTSVFSV--LMVIVGM---GLLLYRRRQKAHF 180

QY 170 PVLVPTQDPPPPSPLLGLKPLQLLEVKARGFGCVWKAQLLNEYVAVKIFPIQDKQSW 229

Db 181 NE-IPTHEAEITNSPPLSNRPQLLEQKASGRFGDVQAKLNQDVAVKIFRMQKESW 239

QY 230 QNEYEYVSLPGMKHENILQFIGAERKGTSDV--VDMLITAFHEKGSLSDFLKANYVSWNQ 288

Db 240 TTEHDYKLPFRMRHPNILEFLGVEKH---MDKPEYWLSTYQHNGSLCDYLKSHTSWPE 296

QY 289 LCHIAETMARGLAYLHEDIPGLK--DGHKPAISHRDITKSNVLLKNNLTACIADFG 347

Db 297 LCRIAESMANGLAHLHEEIPASKTDGLKPSIAHRDFKSNVLLKSDLTACIADFG 356

QY 348 EAGKSAGDTHGOVGTTRYMAPEVELEGAINFQDAFLRIDMYAMGLVWELASRCTA 407

Db 357 QPKPCGDTHGOVGTTRYMAPEVELEGAINFQDAFLRIDMYAMGLVWELASRCTA 415

QY 408 VDEYMLPFEEIQHPSLEDMQEVVYVHKRPVLRDYWKHAGMAMLCETIEECWDHDAE 467

Db 416 VGEFQLPFAELGLRSLDEVOESVYMKLRPRLNLSWRAHPLGVLNFCDTMEECWDHDAE 475

QY 468 AEARLSACVGERITQMRITNIITTEDIVTVMTNVDFPPPKSS 512

Db 476 AEARLSSVCYMERFAQLNKYPS-----TQLLIKHTNID-DAKEST 513

RESULT 5

US-09-878-905-11

; Sequence 11, Application US/09878905

; Patent No. US20020064786A1

; GENERAL INFORMATION:

; APPLICANT: Markowitz, Sanford D

; APPLICANT: Brattain, Michael G

; APPLICANT: Willson, James K.V.

; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND THERAPY BASED ON

; TITLE OF INVENTION: MUTATION OF RECEPTOR

[illegible]

FILE REFERENCE: 062361.0108
; CURRENT APPLICATION NUMBER: US/09/878,905
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 08/417,867
; PRIOR FILING DATE: 1995-04-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 567
; TYPE: PRT
; ORGANISM: human
US-09-878-905-11

Query Match 28.0%; Score 775.5; DB 10; Length 567;
Best Local Similarity 35.6%; Pred. No. 3.2e-55;
Matches 176; Conservative 82; Mismatches 140; Indels 97; Gaps 15;

QY 60 CFATWKNISGSIEIVKQCWLDDINCVD-----RTDCV--EKKDSPEVVF- 102
| | :
DB 84 CVAVWRKNDENITL-----ETVCHDPKLPYHDFILEDAAAPKCIMKEKKKGTEFFM 135
| | :
QY 103 CCCEGNMCNEKFSYPPEMEVTQTSNPVPKPYYNILL-----YSLVPLMLIAGIVI 155
| | :
DB 136 CSCSDECDNDNIIFSEYN---TSPN-----DLLLVIFQVTGISTLLPPLGVASVI 183
| | :
QY 156 CAFWYVRHHUKMAYPPVLPTQDGP PPP-----SPLL 188
| | :
DB 184 IIFYCYRVNRQ---QKLSTWTGTGRKLMFSEHCALIEDDRSDISSCANNINHT 240
| | :
QY 189 LKPLQLLEVKAARGFCVMKAQLLN-----EYVAVKIPIQDKOSQWNEYEVYSLPGMK 242
| | :
DB 241 LLPIELDTLVGKRAEYVAKAKLKONTSEQETVAVKIFFPYEEYASWKTERKDIESDLNK 300
| | :
QY 243 HENILOFGAERKGTSDVDLMLITAFHEKGLSDFLKANYVSNOLCHIAETWARGLAY 302
| | :
DB 301 HENILQFLTAERKETLGQYWLITAFHAKGNLOEYLTRHVLSWEDLRKLGSSLIARIGAH 360
| | :
QY 303 LHEDIPLGDGHKPA-----ISHRDIKSKNVLLKNNLTACTADFGALKFEAGKSAGD- 355
| | :
DB 361 LHSD-----HTPCGRPKMPIVHRDLKSSNLVKNLDLTCCCLDFGLSLRDPTLSVDL 413
| | :
QY 356 -THQVGTTRYMAPEVEGAINFQR-DAPLRIDMYAMGLVWELASRCTAADGPVDEYML 413
| | :
DB 414 ANSGQVGTARYMAPEVLESRMLENESFKQTDVYSMALVLEMTSRCNAV-GEVKDYEP 472
| | :
QY 414 PFEEETGHPSLDMOEVVVHKRPVLDYQKHAGMAMLCETIEECWDHDAEARLSAG 473
| | :
DB 473 PGSKYREHPCVESKMDNVLDRGRPEIPSFNLHQGIQMVCTELTECWHDHDPPEARLTAQ 532
| | :
QY 474 CVGERITQMRLTNI 488
| | :
DB 533 CVAERFSELEHLDR 547
| | :

RESULT 6
US-09-917-788-5
; Sequence 5, Application US/09917788
; Publication No. US20030028905A1
; GENERAL INFORMATION:
; APPLICANT: KNAUS, Rainer
; TITLE OF INVENTION: MUTANT FORMS OF THE TGF-BETA TYPE II RECEPTOR WHICH BIND ALL TGF-
; FILE REFERENCE: ISOFORMS
; CURRENT APPLICATION NUMBER: US/09/917,788
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match 28.0%; Score 775.5; DB 10; Length 1038;
Best Local Similarity 34.5%; Pred. No. 7e-55;
Matches 179; Conservative 103; Mismatches 172; Indels 65; Gaps 19;

QY 60 CFATWKNISGSIEIVKQCWLDDINCVD-----RTDCV--EKKDSPEVVF- 102
| | :
DB 109 CVAVWRKNDENITL-----ETVCHDPKLPYHDFILEDAAAPKCIMKEKKKGTEFFM 160
| | :
QY 103 CCCEGNMCNEKFSYPPEMEVTQTSNPVPKPYYNILL-----YSLVPLMLIAGIVI 155
| | :
DB 161 CSCSDECDNDNIIFSEYN---TSPN-----DLLLVIFQVTGISTLLPPLGVASVI 208
| | :
QY 156 CAFWYVRHHUKMAYPPVLPTQDGP PPP-----SPLL 188
| | :
DB 209 IIFYCYRVNRQ---QKLSTWTGTGRKLMFSEHCALIEDDRSDISSCANNINHT 265
| | :
QY 189 LKPLQLLEVKAARGFCVMKAQLLN-----EYVAVKIPIQDKOSQWNEYEVYSLPGMK 242
| | :
DB 266 LLPIELDTLVGKRAEYVAKAKLKONTSEQETVAVKIFFPYEEYASWKTERKDIESDLNK 325
| | :
QY 243 HENILOFGAERKGTSDVDLMLITAFHEKGLSDFLKANYVSNOLCHIAETWARGLAY 302
| | :
DB 326 HENILQFLTAERKETLGQYWLITAFHAKGNLOEYLTRHVLSWEDLRKLGSSLIARIGAH 385
| | :
QY 303 LHEDIPLGDGHKPA-----ISHRDIKSKNVLLKNNLTACTADFGALKFEAGKSAGD- 355
| | :
DB 386 LHSD-----HTPCGRPKMPIVHRDLKSSNLVKNLDLTCCCLDFGLSLRDPTLSVDL 438
| | :
QY 356 -THQVGTTRYMAPEVEGAINFQR-DAPLRIDMYAMGLVWELASRCTAADGPVDEYML 413
| | :
DB 439 ANSGQVGTARYMAPEVLESRMLENESFKQTDVYSMALVLEMTSRCNAV-GEVKDYEP 497
| | :
QY 414 PFEEETGHPSLDMOEVVVHKRPVLDYQKHAGMAMLCETIEECWDHDAEARLSAG 473
| | :
DB 498 PGSKYREHPCVESKMDNVLDRGRPEIPSFNLHQGIQMVCTELTECWHDHDPPEARLTAQ 557
| | :
QY 474 CVGERITQMRLTNI 488
| | :
DB 558 CVAERFSELEHLDR 572
| | :

RESULT 7
US-09-908-500A-2
; Sequence 2, Application US/0908500A
; Patent No. US20020102576A1
; GENERAL INFORMATION:
; APPLICANT: James Loyd
; APPLICANT: Kirk B. Lane
; APPLICANT: John A. Phillips, III
; TITLE OF INVENTION: METHOD OF DIAGNOSING PULMONARY
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 22000.010803
; CURRENT APPLICATION NUMBER: US/09/908,500A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/218,740
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/220,133
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-500A-2

Query Match 28.0%; Score 775.5; DB 10; Length 1038;
Best Local Similarity 34.5%; Pred. No. 7e-55;
Matches 179; Conservative 103; Mismatches 172; Indels 65; Gaps 19;

Db 363 LKSNILIKKNGSCCIADGLAVKFNSTNEVDVPLNTRVGTFRYMAPEVILDSLKNKHF 422
Qy 378 ORDAFLRIDMYAGMLVWELASRCTAAGPVDEYMLPFEEIEGOHPSLEDQMVVHHKK 437
Db 423 Q-PYMADIYSGLLIWENARCITG-GIVEEYQLPYNNWPSDSYEDMREVVCVKRL 479
Qy 438 RPLVRDYWKHAGMAMLCETIEECWHDHAEARLSAGCVGERITQMORLTNIITEDI 494
Db 480 RPIVSNRWNSECLRAVLKMLSCWAHNPASRLTA-----LRIKKTAKMVESQDV 530
RESULT 10
US-10-153-217-2
; Sequence 2, Application US/10153217
; Publication No. US20030072758A1
; GENERAL INFORMATION:
; APPLICANT: HOWE, JAMES R.
; TITLE OF INVENTION: BMPRIA INVOLVEMENT IN JUVENILE POLYPOSIS
; FILE REFERENCE: IOWA:037US
; CURRENT APPLICATION NUMBER: US/10/153,217
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/292,691
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-153-217-2
Query Match 24.3%; Score 674; DB 9; Length 532;
Best Local Similarity 34.4%; Pred. No. 5.8e-47;
Matches 164; Conservative 86; Mismatches 159; Indels 68; Gaps 15;
Qy 59 HCFATWKNISGIEIVKOGCWLDDINCYDRTDCVEKKDSPEVYFC-----CCEGNCNKEF 114
Db 81 HCFATIEDDQGETTLASGCMK-----YEGSD-FQCKDSPKAQLRRTIECCRTNLCN--- 131
Qy 115 SYFPEMEVTQTSNPVTPKPPY-----YNILLYSLVPLMLIAGIVICAFWVYRHH----- 164
Db 132 -----QYLOPTLPVPIVGGFSGIRWLVLISMA-VCIAMIIFSSFCFCYKHYCKSIS 184
Qy 165 -----KMAYPV-----LVPTQDGP PPPPLIG-----LKPLQLLEVKRGR 202
Db 185 SRRYNRDLQDEAFIPVGSGLDLIDQSSGSGGLPLLQVRTAKQIQMVQVQKGR 244
Qy 203 FGCVWKAQLLNEYVAVKIFPIQDKQSWQNEYVYSLPGMKHENILQFIAGKRGTSVDVD 262
Db 245 YGEVWNGKRGKAVKVFETTESAFRETEIYQTVLMRHNILGFIADIKGTGTSWTQ 304
Qy 263 LWLITAPHEKGSLSDFLKANVSVNQNLCHTAETWARGLAVLHEDIPGLKDGHPATSHRD 322
Db 305 LYLTIDYHENGSLYDFLKCATFLDTRALLKLAISAACGLCHLHTEIYGTQ--KPAIAHRD 362
Qy 323 IKSNNVLLKNNLTACIADFGALAFKAGKSAGDT--HGQVGTTRYMAPEVLEGAIN---F 377
Db 363 LKSNILIKKNGSCCIADGLAVAFNSDNEVDVPLNTRVGTFRYMAPEVILDSLKNKHF 422
Qy 378 ORDAFLRIDMYAGMLVWELASRCTAAGPVDEYMLPFEEIEGOHPSLEDQMVVHHKK 437
Db 423 Q-PYMADIYSGLLIWENARCITG-GIVEEYQLPYNNWPSDSYEDMREVVCVKRL 479
Qy 438 RPLVRDYWKHAGMAMLCETIEECWHDHAEARLSAGCVGERITQMORLTNIITEDI 494
Db 480 RPIVSNRWNSECLRAVLKMLSCWAHNPASRLTA-----LRIKKTAKMVESQDV 530
RESULT 11
US-09-903-068-6
; Sequence 6, Application US/09903068

; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten; Frautzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-903-068-6
Query Match 24.3%; Score 674; DB 10; Length 532;
Best Local Similarity 34.4%; Pred. No. 5.8e-47;
Matches 164; Conservative 86; Mismatches 159; Indels 68; Gaps 15;
Qy 59 HCFATWKNISGIEIVKOGCWLDDINCYDRTDCVEKKDSPEVYFC-----CCEGNCNKEF 114
Db 81 HCFATIEDDQGETTLASGCMK-----YEGSD-FQCKDSPKAQLRRTIECCRTNLCN--- 131
Qy 115 SYFPEMEVTQTSNPVTPKPPY-----YNILLYSLVPLMLIAGIVICAFWVYRHH----- 164
Db 132 -----QYLOPTLPVPIVGGFSGIRWLVLISMA-VCIAMIIFSSFCFCYKHYCKSIS 184
Qy 165 -----KMAYPV-----LVPTQDGP PPPPLIG-----LKPLQLLEVKRGR 202
Db 185 SRRYNRDLQDEAFIPVGSGLDLIDQSSGSGGLPLLQVRTAKQIQMVQVQKGR 244
Qy 203 FGCVWKAQLLNEYVAVKIFPIQDKQSWQNEYVYSLPGMKHENILQFIAGKRGTSVDVD 262


```

: ATTORNEY/AGENT INFORMATION:
:
: NAME: LAZAR, Steven R
:
: REGISTRATION NUMBER: 32,618
:
: REFERENCE/DOCKET NUMBER: 5203
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 617 876 1170
:
: TELEFAX: 617 876 5851
:
: INFORMATION FOR SEQ ID NO: 2:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 532 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-874,628-2

```

[illegible]

```

RESULT 14
US-10-044-716-14
; Sequence 14, Application US/10044716
; Patent No. US20020159986A1
; GENERAL INFORMATION:
; APPLICANT: LANGENFELD, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PR
; FILE REFERENCE: 270/070US
; CURRENT APPLICATION NUMBER: US/10/044,716
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

```

```

; LOCATION: (367)..(606)
; OTHER INFORMATION: Activin_recpt; Region: Activin types I and II
; NAME/KEY: misc_feature
; LOCATION: (883)..(1746)
; OTHER INFORMATION: pkinase; region: Eukaryotic protein kinase domain
; NAME/KEY: misc_feature
; LOCATION: (883)..(1746)
; OTHER INFORMATION: TyrKc; Region: Tyrosina kinase, catalytic domain
; NAME/KEY: misc_feature
; LOCATION: (883)..(1725)
; OTHER INFORMATION: TKC; Region: Serine/Threonine protein kinases, catalytic domain
US-10-044-716-14

Query Match      23.6%; Score 653.5; DB 9; Length 502;
Best Local Similarity 34.5%; Pred. No. 2.6e-45;
Matches 161; Conservative 81; Mismatches 170; Indels 55; Gaps

QY 59 HCFATWKNIGSGEIVKQGW---LDDINCYDRDCEVKDKDSPEVFCCEGNCMEKFS 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 YCFYTMIEDSDGLPVVTSGSGLEGSGDFQCRD-TPIPHQRRSIE---CCTERNECNKL- 106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 YFPEMEVQTPTSNPVTK-----PPYINLLYSLV---PLMLIAGIVICAFWVRHH--- 164
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 -----HFTPLPLKNRDFVDGPIHRALLISVTVCSLLLVLLILFCYFYRKQETRRP 158
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 -----KWAYPP-----VLVPTQDPGPPPPSPLLG-----LKPLQLLEVKARGFGCV 206
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 YSIGLEQDETYIPGESLRDLIEQSQSGSGGLPLLVQRTIAKIQMVKQICKGRYGEV 218
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 WKAQLLNEYAVKFIPTQDKSQWNEVEVYSLGPKMHENILQFIGAEKRTSDVDVLWLI 266
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 WMGKWRGEKVAVKVFTEESAMPREFTEIYOTVLMRHENILGFTIAADIKGTGSMWTOLYI 278
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 267 TAFHEKSGSLDFLKANVSVNNQLCHIAETMARGLAYLHEDIPLGDKGHKPAISHRIDKSK 326
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 279 TDYHENGSLDYLKSTTLDKASKMLKAYSSVSGLCHLHTEI---FSTQCKPAIAHRDLKSK 336
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 NVLLKNLNTACIADFGIALKFEAGKSAGD---THGQVGTTRYMAPEVLGAIN---FORDA 381
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 NILVKNGTCCCIADGLGAVAKFISDTNEVDIPPPTRVGTGRYMPPEVLDESINRHHFQ--S 394
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 382 FLRTIDVAMGLVWELASRCAADGPVDEYMLPFEEIEIGHPSLEDMQEVVVVHKRPVL 441
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 395 YIMADMTSFGLLIWEVARRCVSG-GIVEEFQLPVHDLVPSDPSYEDMRREIVCICKLRPSF 453
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 442 RDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERITQMQLNTNI 488
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 454 PNRWSSDECIROMGKLMTECAWNPASRLTALRVKKTFLAKMSFSDI 500
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 15
US-09-874-628-4
; Sequence 4, Application US/09874628
; Patent No. US20020137133A1
; GENERAL INFORMATION:
APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. US20020137133A1orU
TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute Inc.- Legal Affairs
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0.
; Version #1.25

```

Search completed: May 10, 2003, 18:01:05
Job time : 26 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 17:56:45 ; Search time 16 seconds
(without alignments)
943.372 Million cell updates/sec

Title: US-09-742-684A-16

Perfect score: 2770

Sequence: 1 MGAARKLAFAPVLCSSGA.....IVTVMTVNDVFPKESL 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2763	99.7	513	2	US-08-357-533A-10
2	2763	99.7	513	2	US-08-459-009-10
3	2763	99.7	513	2	US-08-300-584-2
4	2763	99.7	513	3	US-08-459-951-10
5	2763	99.7	513	4	US-08-738-168B-13
6	2763	99.7	513	4	US-08-476-123-2
7	2749	99.2	521	4	US-08-738-168B-5
8	2482.5	89.6	514	4	US-08-738-168B-15
9	1971.5	71.2	510	2	US-08-300-584-4
10	1971.5	71.2	510	2	US-08-476-123-4
11	1931	69.7	536	2	US-08-357-533A-12
12	1931	69.7	536	2	US-08-459-009-12
13	1931	69.7	536	3	US-08-459-951-12
14	1915.5	69.2	513	2	US-08-357-533A-11
15	1915.5	69.2	513	2	US-08-459-009-11
16	1915.5	69.2	513	3	US-08-459-951-11
17	1702	61.4	323	3	US-08-158-735A-12
18	1147.5	41.4	516	2	US-08-357-533A-2
19	1147.5	41.4	516	2	US-08-459-009-2
20	1147.5	41.4	516	3	US-08-459-951-2
21	775.5	28.0	567	1	US-08-361-873A-2
22	775.5	28.0	567	2	US-08-483-926A-1
23	775.5	28.0	567	2	US-08-854-768-1
24	775.5	28.0	567	2	US-08-445-520B-9
25	775.5	28.0	567	2	US-08-737-045-1
26	775.5	28.0	567	3	US-08-451-946B-8
27	775.5	28.0	567	3	US-08-446-938B-8

28 775.5 28.0 567 3 US-08-311-703A-8 Sequence 8, Appli
29 775.5 28.0 567 3 US-08-446-938B-8 Sequence 8, Appli
30 775.5 28.0 567 3 US-09-183-543-8 Sequence 8, Appli
31 775.5 28.0 567 4 US-08-446-936A-8 Sequence 8, Appli
32 775.5 28.0 567 4 US-09-239-864A-11 Sequence 11, Appli
33 775.5 28.0 567 5 PCT-US92-09326-4 Sequence 4, Appli
34 775.5 28.0 582 4 US-08-334-179A-4 Sequence 4, Appli
35 775.5 28.0 1038 4 US-08-334-179A-2 Sequence 2, Appli
36 770.5 27.8 1038 4 US-08-334-179A-8 Sequence 8, Appli
37 731.5 26.4 565 2 US-08-357-533A-9 Sequence 9, Appli
38 731.5 26.4 565 2 US-08-459-009-9 Sequence 9, Appli
39 731.5 26.4 565 3 US-08-459-951-9 Sequence 9, Appli
40 717.5 25.9 325 4 US-08-158-735A-13 Sequence 13, Appli
41 674 24.3 532 2 US-08-481-337A-6 Sequence 6, Appli
42 674 24.3 532 4 US-08-382-256-6 Sequence 6, Appli
43 674 24.3 532 4 US-09-395-115-6 Sequence 6, Appli
44 674 24.3 532 4 US-08-436-265-6 Sequence 6, Appli
45 674 24.3 532 4 US-09-679-187-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-357-533A-10
; Sequence 10, Application US/08357533A
; Patent No. 5831050
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,533A
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-073FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)-435-9001
; TELEFAX: (508)-435-0992
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..513
; OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"
US-08-357-533A-10

Query Match 99.7%; Score 2763; DB 2; Length 513;
Best Local Similarity 99.4%; Pred. No. 6.2e-264;

Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGAAGLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGPEYCGDKDKRRHC 60
DB 1 MGAAGLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGPEYCGDKDKRRHC 60
QY 61 FATWKNISGSIIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
DB 61 FATWKNISGSIIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
DB 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
QY 181 PPPSLGLGLKPLQLLEVKARFGCVKQAQLLNEYVAVKIPFIQDKQSWQNEYEYVSLPG 240
DB 181 PPPSLGLGLKPLQLLEVKARFGCVKQAQLLNEYVAVKIPFIQDKQSWQNEYEYVSLPG 240
QY 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGL 300
DB 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNLTACTIADFGALKFEAGKSAGDTHGOV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNLTACTIADFGALKFEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEIG 420
DB 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEIG 420
QY 421 QHPSLEDMDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDMDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVTNVDPPKESL 513
DB 481 QMORLTNIITTEDIVVTVMVTNVDPPKESL 513
```

RESULT 2

```
US-08-459-009-10
; Sequence 10, Application US/08459009
; Patent No. 5861479
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,009
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,533
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
```

REFERENCE/DOCKET NUMBER: CRP-073FW

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)-435-9001
; TELEFAX: (508)-435-0992
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..513
; OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"
US-08-459-009-10
```

Query Match 99.7%; Score 2763; DB 2; Length 513;

Best Local Similarity 99.4%; Pred. No. 6.2e-264; Mismatches 3; Indels 0; Gaps 0; Matches 510; Conservative 3;

```
QY 1 MGAAGLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGPEYCGDKDKRRHC 60
DB 1 MGAAGLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGPEYCGDKDKRRHC 60
QY 61 FATWKNISGSIIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
DB 61 FATWKNISGSIIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNNMCNEKFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
DB 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
QY 181 PPPSLGLGLKPLQLLEVKARFGCVKQAQLLNEYVAVKIPFIQDKQSWQNEYEYVSLPG 240
DB 181 PPPSLGLGLKPLQLLEVKARFGCVKQAQLLNEYVAVKIPFIQDKQSWQNEYEYVSLPG 240
QY 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGL 300
DB 241 MKHENILOFIGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNLTACTIADFGALKFEAGKSAGDTHGOV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNLTACTIADFGALKFEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEIG 420
DB 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAMGLVWLWELASRCTAADGPVDEYMLPFEEIG 420
QY 421 QHPSLEDMDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDMDQEVVYVHKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVTNVDPPKESL 513
DB 481 QMORLTNIITTEDIVVTVMVTNVDPPKESL 513
```

RESULT 3

```
US-08-300-584-2
; Sequence 2, Application US/08300584
; Patent No. 5885794
; GENERAL INFORMATION:
; APPLICANT: Mathews, Lawrence S.
; APPLICANT: Vale, Wylie W.
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
```

COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,584
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/880,220
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/773,229
FILING DATE: 09-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,709
FILING DATE: 10-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-300-584-2

Query Match 99.7%; Score 2763; DB 2; Length 513;
Best Local Similarity 99.4%; Pred. No. 6.2e-264;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGVPCYGDKKRRHC 60
DB 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGVPCYGDKKRRHC 60
QY 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
DB 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
QY 121 EVTQPTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
DB 121 EVTQPTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
QY 181 PPPSPLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKOSQWNEYEYVSLPG 240
DB 181 PPPSPLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKOSQWNEYEYVSLPG 240
QY 241 MKHENILOFIGAEGKRGTSVDVLDWLITAFHEKGSLSDFLKANYVSNWOLCHIAETMARGL 300
DB 241 MKHENILOFIGAEGKRGTSVDVLDWLITAFHEKGSLSDFLKANYVSNWOLCHIAETMARGL 300
QY 301 ATYLEDIPGLKDGHPALSHRDIDSKNVLKNNLTACTADTGLALKFEAGSAGDTHGQV 360
DB 301 ATYLEDIPGLKDGHPALSHRDIDSKNVLKNNLTACTADTGLALKFEAGSAGDTHGQV 360
QY 361 GTRRYMAPEVLEGAINFOADFLRDMYAGLVLEWLASRCTAADGPDVYMLPFEIEIG 420
DB 361 GTRRYMAPEVLEGAINFOADFLRDMYAGLVLEWLASRCTAADGPDVYMLPFEIEIG 420
QY 421 QHPSLEDQEVVHVKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDQEVVHVKKRPVLDYWKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVTVVTVMTNVDFPPKSSSL 513
DB 481 QMORLTNIITTEDIVTVVTVMTNVDFPPKSSSL 513

DB 481 QMORLTNIITTEDIVTVVTVMTNVDFPPKSSSL 513
RESULT 4
US-08-459-951-10
Sequence 10, Application US/08459951
Patent No. 6093547
GENERAL INFORMATION:
APPLICANT: JIN, DONALD F
APPLICANT: OPPERMAN, HERMANN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: SMART, JOHN E
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
ADDRESSEE: INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,951
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,533
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-073FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1-513
OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"
US-08-459-951-10

Query Match 99.7%; Score 2763; DB 3; Length 513;
Best Local Similarity 99.4%; Pred. No. 6.2e-264;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGVPCYGDKKRRHC 60
DB 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGVPCYGDKKRRHC 60
QY 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
DB 61 FATWKNISGSIEIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
QY 121 EVTQPTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
DB 121 EVTQPTSNPVTPKPPYYNLLYSVLPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
QY 181 PPPSPLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKOSQWNEYEYVSLPG 240
DB 181 PPPSPLGLKPLQLLEVKARGFGCVKWAQLLNEYVAVKIFPIQDKOSQWNEYEYVSLPG 240

QY 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNSWNLCHIAETMARGL 300
DB 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNSWNLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQV 360
QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEIEIG 420
DB 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEIEIG 420
QY 421 QHPSLEDMQEVVVVHKKRPVLDYQKHWAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDMQEVVVVHKKRPVLDYQKHWAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLNIITTEDIVTVVMTNVDPPKESL 513
DB 481 QMORLNIITTEDIVTVVMTNVDPPKESL 513

RESULT 5

-08-738-168B-13

Sequence 13, Application US/08738168B

Patent No. 6132988

GENERAL INFORMATION:

APPLICANT: Sugino, Hiromu

APPLICANT: Nakamura, Takanori

APPLICANT: Shouji, Hiroki

TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,168B

FILING DATE: 25-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 280939/1995

FILING DATE: 27-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 174909/1996

FILING DATE: 04-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Resnick, David S.

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 342/46901

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 513 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-738-168B-13

Query Match 99.78; Score 2763; DB 4; Length 513;
Best Local Similarity 99.48; Pred. No. 6.2e-264;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLSCSSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKDKRRHC 60

DB 1 MGAALKAFVFLSCSSGAILGRSETQCLFFNANWEKDRNTQGVPCYGDKDKRRHC 60
QY 61 FATWKNISGSIIVKQGCWLDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKESYFPEM 120
DB 61 FATWKNISGSIIVKQGCWLDINCYDRTDCIEKKDSPEVYFCCCEGNCNEKESYFPEM 120
QY 121 EYQTPSNVTPKPPYNNILLYSLVPLMLIAGIVICAFWVYRHHKMMAYPPVLVPTQDGP 180
DB 121 EYQTPSNVTPKPPYNNILLYSLVPLMLIAGIVICAFWVYRHHKMMAYPPVLVPTQDGP 180
QY 181 PPPSPLLGLKPLQLLEVARGFCGWKAQLNVEYVAVKIPIQDKQSWQNEIEYVSLPG 240
DB 181 PPPSPLLGLKPLQLLEVARGFCGWKAQLNVEYVAVKIPIQDKQSWQNEIEYVSLPG 240
QY 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNSWNLCHIAETMARGL 300
DB 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNSWNLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQV 360
DB 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALAKFEAGKSAGDTHGQV 360
QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEIEIG 420
DB 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEIEIG 420
QY 421 QHPSLEDMQEVVVVHKKRPVLDYQKHWAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
DB 421 QHPSLEDMQEVVVVHKKRPVLDYQKHWAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
QY 481 QMORLNIITTEDIVTVVMTNVDPPKESL 513
DB 481 QMORLNIITTEDIVTVVMTNVDPPKESL 513

RESULT 6

US-08-476-123-2

Sequence 2, Application US/08476123

Patent No. 6162896

GENERAL INFORMATION:

APPLICANT: Mathews, Lawrence S.

APPLICANT: Vale, Wylie W.

APPLICANT: Tsuchida, Kunihiro

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,123

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/485,061

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/300,584

FILING DATE: 02-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/880,220

FILING DATE: 08-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/773,229

FILING DATE: 09-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,709
FILING DATE: 10-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9927
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-123-2

Query Match 99.7%; Score 2763; DB 4; Length 513;
Best Local Similarity 99.4%; Pred. No. 6.2e-264;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
DB 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
QY 61 FATWKNISGSEIVKQGCWLDLINCIDRTDCVEKKDSPEVYFCCCGNMCNEKESYFPEM 120
DB 61 FATWKNISGSEIVKQGCWLDLINCIDRTDCIEKKDSPEVYFCCCGNMCNEKESYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
DB 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
QY 181 PPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKQSWQNEYEVSLEPG 240
DB 181 PPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKQSWQNEYEVSLEPG 240
QY 241 MKHENILQFAGKRGTSVDVLDLWLTAFHEKGSLSDFLKNVSNQCHIAETMARGL 300
DB 241 MKHENILQFAGKRGTSVDVLDLWLTAFHEKGSLSDFLKNVSNQCHIAETMARGL 300
QY 301 AYLEDIPGLKDGHKPAISHRDIKSNVLLKNLTACIADFGALAKFEAGKSAGDTHGOV 360
DB 301 AYLEDIPGLKDGHKPAISHRDIKSNVLLKNLTACIADFGALAKFEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVEGAIFNFORDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETG 420
DB 361 GTRRYMAPEVEGAIFNFORDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETG 420
QY 421 QHPSLEDQMVVYHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCGVERT 480
DB 421 QHPSLEDQMVVYHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSAGCGVERT 480
QY 481 QMORLNIITTEDIVTVMTNVDPPPKESL 513
DB 481 QMORLNIITTEDIVTVMTNVDPPPKESL 513

RESULT 7
US-08-738-168B-5
Sequence 5, Application US/08738168B
Patent No. 6132988
GENERAL INFORMATION:
APPLICANT: Sugino, Hiromu
APPLICANT: Nakamura, Takao
APPLICANT: Shouji, Hiroki
TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street

CITY: Boston
STATE: MA USA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,168B
FILING DATE: 25-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280939/1995
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 174909/1996
FILING DATE: 04-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 342/46901
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-168B-5

Query Match 99.2%; Score 2749; DB 4; Length 521;
Best Local Similarity 97.9%; Pred. No. 1.5e-262;
Matches 510; Conservative 3; Mismatches 0; Indels 8; Gaps 1;

QY 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
DB 1 MGAALKAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQTVGPCYGDKDKRRHC 60
QY 61 FATWKNISGSEIVKQGCWLDLINCIDRTDCVEKKDSPEVYFCCCGNMCNEKESYFPEM 120
DB 61 FATWKNISGSEIVKQGCWLDLINCIDRTDCIEKKDSPEVYFCCCGNMCNEKESYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQ 176
DB 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQ 180
QY 177 ----DPGPPPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKQSWQNE 232
DB 181 IMIEDPGPPPSPLGLKPLQLLEVKARGCGVWKAQLLNEYVAVKIFPIQDKQSWQNE 240
QY 233 YEVYSLPQMKHENILQFAGKRGTSVDVLDLWLTAFHEKGSLSDFLKNVSNQCHIA 292
DB 241 YEVYSLPQMKHENILQFAGKRGTSVDVLDLWLTAFHEKGSLSDFLKNVSNQCHIA 300
QY 293 AETMARGLAYLHEDIPGLKDGHKPAISHRDIKSNVLLKNLTACIADFGALAKFEAGKS 352
DB 301 AETMARGLAYLHEDIPGLKDGHKPAISHRDIKSNVLLKNLTACIADFGALAKFEAGKS 360
QY 353 AGDTHGOVTRRYMAPEVEGAIFNFORDAFLRIDMYAMGLVWELASRCTAADGPVDEYM 412
DB 361 AGDTHGOVTRRYMAPEVEGAIFNFORDAFLRIDMYAMGLVWELASRCTAADGPVDEYM 420
QY 413 LPFEEIIGQHPSELEDQMVVYHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSA 472
DB 421 LPFEEIIGQHPSELEDQMVVYHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARLSA 480
QY 473 GCVERITQMORLNIITTEDIVTVMTNVDPPPKESL 513
DB 481 GCVERITQMORLNIITTEDIVTVMTNVDPPPKESL 521

Tue May 13 17:51:40 2003

RESULT 8
US-08-738-168B-15
; Sequence 15 Application US/08738168B
; Patent No. 6132988
; GENERAL INFORMATION:
; APPLICANT: Sugino, Hiromu
; APPLICANT: Nakamura, Takanori
; APPLICANT: Shouji, Hiroki
; TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,168B
; FILING DATE: 25-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280939/1995
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 174909/1996
; FILING DATE: 04-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 342/46901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-738-168B-15

Query Match 89.6%; Score 2482.5; DB 4; Length 514;
Best Local Similarity 87.7%; Pred. No. 2.9e-236;
Matches 451; Conservative 37; Mismatches 25; Indels 1; Gaps 1;

1 MGAATAKLAFAVFLSCSS-GAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKRRH 59
1 MGAATKLAFAVFLSCSSAGSILGRSETKECIYYNANWEKDKTNSNGTEICYGDNDRKH 60

60 CFATWKNISGSEIIVKQCWLLDDINCVDRTDCVEKDSPEVYFCCCGNMCNEKFSYFE 119
61 CFATWKNISGSEIIVKQCWLLDDINCYNKSKTEKKKSPDVFCCCGNCKNEKFSYFE 120

120 MEVTOPTSNVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHKMAYPVPLVPTQDPG 179
121 MEVTOPTSNVTPKPPYNNILLYSLVPLMVAVIVLSFWMYRHHKLAYPPVPLVPTQDPG 180

180 PPPPSPLGLKPLQLLEVKARGCGVWKAQLINNEYAVKIFPIODKQSNQNEYEYSLP 239
181 PPPPSPLGLKPLQLLEVKARGCGVWKAQLINNEYAVKIFPIODKQSNQNEYEYSLP 240

240 GKNHENILQFIGAEKRGTSVDVDLWLTAFHEKGSLSDFLKNVYSNNOLCHIAETNARG 299
241 GKNHENILQFIGAEKRGTSVDVDLWLTAFHEKGSLSDFLKNVYSNNOLCHIAETNARG 300

300 LAYLHEDIPGLKDGHPKPAISHRDIKSKNVLLKNNLTACIADFGALAKFEAGKSAGDTHGQ 359
1:|||||

Db 301 LSHLHEDIPGLKDGHPKPAISHRDIKSKNVLLKNNLTACIADFGALAKFEAGKSAGDTHGQ 360
QY 360 VGTTRYMAPEVLEGAINFQDAFLRIDMYAGLVWELASRCTAADGPDVEYMLPFEEI 419
Db 361 VGTTRYMAPEVLEGAINFQDAFLRIDMYAGLVWELASRCTASDGPVDEYMLPFEEV 420
QY 420 GQHSLEDMDQEVVYHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
Db 421 GQHSLEDMDQEVVYHKKRPVLRDYWKQKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 480
QY 480 TOMQRLTNIIITEDIVTV 513
Db 481 TOMQRLTNIIITEDIVTV 514

RESULT 9
US-08-300-584-4
; Sequence 4, Application US/08300584
; Patent No. 5885794
; GENERAL INFORMATION:
; APPLICANT: Mathews, Lawrence S.
; APPLICANT: Vale, Wylie W.
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,584
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,220
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/773,229
; FILING DATE: 09-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,709
; FILING DATE: 10-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-9392
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 510 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-300-584-4

Query Match 71.2%; Score 1971.5; DB 2; Length 510;
Best Local Similarity 67.9%; Pred. No. 7.1e-186;
Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

1 MGAATAKLAFAVFLSCSSGAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDKRRHC 60
1 MGASVALTFULLLATFRAGSHDEVTRECIYYNANWEKDKTNSNGTEICYGDNDRKH 60

Qy	61	PATWKNISGSIETIVKQGCWLDDINCVDRTDCEVKKDSPEYVIFCCCGNMCNEKESFYFPEM	120
Db	61	YASRNNSGFIELVKKQGCWLDDFNCQROECIAKENPVFFCCCGNCKNKKFTLPEV	120
Qy	121	EVTOPTSNVTPKPPYYNILLYSVLPLMLTAGIVICAFNYYRHHKWAYPPVLVPTDOPG	180
Db	121	ETFDPRQ---PSNSVLNIIYSLLFVLGSLMAILAFNRIHRKPPYGHVEI-NDPGL	176
Qy	181	PPSPPLGLQLLOLVKARGCGVWKQAOLLNEYVAVKIFPQDKOSQWNEYEYVSLPG	240
Db	177	PPSPVLGLQLLOLLETIKARGCGVWKARLLNEYVAVKIFPVQDKOSWQCEKEIFTTPG	236
Qy	241	MKENILQFIAGSKRGTSVDVLDWLITAPHEKGSLSDFLKANVYVSNQJLCHAEIMARG	300
Db	237	MKENLEFTAERKSGNSLDEDLWLITAPHDKGLTDYLUKNVLSWNEJCHTETIMARG	296
Qy	301	AYLHEDIPGLK-DGHRPAISHRDIKSNVLLKNNLACIADFGALKEAGKSAGDTHQ	359
Db	297	AYLHEDVPRCGECHKPAIAHROFKSNVLLRNDLTAIADFGCLAVREFPGKPPGDTHQ	356
Qy	360	VGTRRYMAPEVLGSAINFODAFLRDMYAMGLVILWELASRCTAADGPVDEYMLPFEEI	419
Db	357	VGTRRYMAPEVLGSAINFODSFLRDMYAMGLVILWEIVSRCTAADGPVDEYLLPFEEI	416
Qy	420	GQHPSLDMQEVVVVHKKRPVLRYDQWKHAGMAMLCETIEECWHDDAEARLSAGCVGERI	479
Db	417	GQHPSLDLQEVVVVHKKRPVFKDHLWKHPGLAQLCVTIEECWHDDAEARLSAGCVGERI	476
Qy	480	TQWRLTNITTEDIVVTVMVTNVDPPKRESSL	513
Db	477	SQIRKSVNGTSDCLVTSIVTNSVDLPPKRESSI	510

RESULT 10
 US-08-476-123-4
 ; Sequence 4, Application US/08476123
 ; Patent No. 6162896
 ; GENERAL INFORMATION:
 ; APPLICANT: Mathews, Lawrence S.
 ; APPLICANT: Vale, Wylie W.
 ; APPLICANT: Tsuchida, Kunihiro
 ; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
 ; TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/476,123
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/485,061
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/300,584
 ; FILING DATE: 02-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/880,220
 ; FILING DATE: 08-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/773,229
 ; FILING DATE: 09-OCT-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/698,709

[illegible]

RESULT 11
 US-08-357-533A-12
 ; Sequence 12, Application US/08357533A
 ; Patent No. 5831050
 ; GENERAL INFORMATION:
 ; APPLICANT: JIN, DONALD F
 ; APPLICANT: OPPERMANN, HERMANN
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; APPLICANT: SMART, JOHN E
 ; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
 ; ADDRESSEE: INC
 ; STREET: 45 SOUTH STREET
 ; CITY: HOPKINTON

```

NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-073FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..536
OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II
OTHER INFORMATION: RECEPTOR"
US-08-459-009-12

Query Match          69.7%; Score 1931; DB 2; Length 536;
Best Local Similarity 64.7%; Pred. No. 7.5e-182;
Matches 343; Conservative 86; Mismatches 77; Indels 24; Gaps

Qy      8  AFAPVLISCSGAILGRSETQECILFFNANKEKDRKTNOTGVPCYGDKDRRHCFATWKNI 67
Db      7  ALALLWSLCAAGSRGAEATRECIYYNANWELERTNQSGLERCEGQDKRLHCYASWANS 66
Qy      68  SGSTEIVKQGWLDDINCYDRTDCVEKKSDPEYVFCCEGNCMCNEKFSVPPEMVEVTOPTS 127
Db      67  SGTIELVKKGWLLDDFNCYDRQECVATEEPQVTFCCCEGNCNERFTHLPEPGGPEVTV 126
Qy      128  NPVTPKPPYYNILLYSVLPLMLIAGIVICAFWYVRHKKMAYPPVLV----- 173
Db      127  EPPPTATLLTVLAYSLIPGGLSLIVLLAFWVYRHKPPYGHVDIHEVRQCQRWAGRRD 186
Qy      174  -----PTQDPGPPPPSLGLKPLQLLELVKARGFCGVKWAQLLNYYAVKIFPTQ 224
Db      187  GCADSFKPLPDODGPPPPSLVGLKPLQLLELVKARGFCGVKWAQLMNDFAVKIFPLQ 246

```

QY 225 DKQSWNEYEYVSLPGMKHNLQFTCAEKRGTSDVDLWLTAFHEKGLSDFELKANV 284
Db 247 DKQSWSEREIFSTPGMKHNLQFTCAEKRGTSDVDLWLTAFHEKGLSDFELKANV 306
QY 285 SWNOLCHIAETMARGLAYLHEDIPGLK-DGHPAISHRDIKSKNVLKNNLTACTADFG 343
Db 307 TWNELCHVAETMSRGLSYLHEDVPCWGEHGHKPSIAHRDFKSKNVLKSDLTAVLADFG 366
QY 344 ALFAEAGKAGDTHGQVTRRYMAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCTA 403
Db 367 AVFEFGKPGDTHGQVTRRYMAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCKA 426
QY 404 ADGPVDEYMLPFEETIQHPSLEDMQEVVYVHKRPVLDYQKAGMAMLCETIEECWD 463
Db 427 ADGPVDEYMLPFEETIQHPSLEELQEVVYVHKMRPTIKDHWLKHPLGIAQLCVTIEECWD 486
QY 464 HDAEARLSAGCGVGRITOMORLTNIITTEDIVTVMTNVDPFPKESL 513
Db 487 HDAEARLSAGCVERSLIRSVNGTSDCLVSLVTSVTNVDDLKPESSI 536

RESULT 13
US-08-459-951-12
; Sequence 12, Application US/08459951
; Patent No. 6093547
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08459,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,533
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-073FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)-435-9001
; TELEFAX: (508)-435-0992
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..536
; OTHER INFORMATION: /note="HUMAN ACTIVIN TYPE II
; OTHER INFORMATION: RECEPTOR"

US-08-459-951-12

Query Match 69.7% Score 1931; DB 3: Length 536;
Best Local Similarity 64.7% Pred. No. 7.5e-182;
Matches 343; Conservative 86; Mismatches 77; Indels 24; Gaps 2;
QY 8 AFAPVLISSCGSAILGRSETQECLEFFNANWEKDRDTNOTGVPCYGDKKRRHCFATWKN 67
Db 7 ALALLWGLSAGSGRGEAETRECIYVYNNANWELERTNSGLERCEGEQDKRLHCVASWNS 66
QY 68 SGSTEIVKQGWLDINDICYDRDCEVKEKSDPEVYFCCCEGNNCKEFSYPPEMEVTP 127
Db 67 SGTIELVKKGWLDNFCYDRQECVATEENPQVYFCCCEGNNCFNERETHLPEPGGPEV 126
QY 128 NPVTPKPPYNYLLYSVPLMLIAGIVICAFVWRHMKMAYPPVLV----- 173
Db 127 EPPPTAPTLVLLVAYSLPLPGGLSLVLLAFWMTYHRRKPPYGHVDDIIEVROCQRWARR 186
QY 174 -----PTQDPGPPPPSLLGLKPLQLLEVKARGFCVWKRAQLLNVEYVAYKIFPIQ 224
Db 187 GCADSFKPLPQDPGPPPPSPLVGLKPLQLLEIKARGFCVWKRAQLMDFVAVKIFPLQ 246
QY 225 DKQSWNEYEYVSLPGMKHNLQFTCAEKRGTSDVDLWLTAFHEKGLSDFELKANV 284
Db 247 DKQSWSEREIFSTPGMKHNLQFTCAEKRGTSDVDLWLTAFHEKGLSDFELKANV 306
QY 285 SWNOLCHIAETMARGLAYLHEDIPGLK-DGHPAISHRDIKSKNVLKNNLTACTADFG 343
Db 307 TWNELCHVAETMSRGLSYLHEDVPCWGEHGHKPSIAHRDFKSKNVLKSDLTAVLADFG 366
QY 344 ALFAEAGKAGDTHGQVTRRYMAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCTA 403
Db 367 AVFEFGKPGDTHGQVTRRYMAPEVLEGAINFORDAFRLIDMYAMGLVWELASRCKA 426
QY 404 ADGPVDEYMLPFEETIQHPSLEDMQEVVYVHKRPVLDYQKAGMAMLCETIEECWD 463
Db 427 ADGPVDEYMLPFEETIQHPSLEELQEVVYVHKMRPTIKDHWLKHPLGIAQLCVTIEECWD 486
QY 464 HDAEARLSAGCGVGRITOMORLTNIITTEDIVTVMTNVDPFPKESL 513
Db 487 HDAEARLSAGCVERSLIRSVNGTSDCLVSLVTSVTNVDDLKPESSI 536

RESULT 14
US-08-357-533A-11
; Sequence 11, Application US/08357533A
; Patent No. 5831050
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,533A
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-073FW

Page 11

Search completed: May 10, 2003, 18:00:34
Job time : 18 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 17:55:10 ; Search time 21 Seconds
(without alignments)
2348.427 Million cell updates/sec

Title: US-09-742-684a-16
Perfect score: 2770
Sequence: 1 MGAALAFAPVELISCSSGA.....IVTVVTMTNVDFPPRESSL 513
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2767	99.9	513	JQ1486	activin receptor I
2	2763	99.7	513	A39896	activin receptor p
3	2762	99.7	513	S27258	activin receptor t
4	2759	99.6	513	A49193	type II activin re
5	2743	99.0	513	I43850	activin receptor t
6	2604	94.0	513	S23089	activin receptor t
7	2482.5	89.6	514	JQ1317	activin receptor p
8	2474.5	89.3	512	S21171	activin receptor S
9	1971.5	71.2	510	A42635	activin receptor S
10	1965.5	71.0	510	A56926	activin receptor I
11	1940	70.0	512	I37134	activin type II re
12	1935	69.9	512	D40829	activin receptor i
13	1934	69.8	536	A40829	activin receptor i
14	1923	69.4	504	B40829	activin receptor i
15	1922	69.4	528	C40829	activin receptor i
16	1915.5	69.2	513	JQ1484	activin receptor p
17	1472	53.1	382	A49193	type II activin re
18	1312.5	47.4	365	S27268	activin receptor S
19	1147.5	41.4	516	A48678	activin receptor I
20	1051	37.9	251	PC4261	activin type II re
21	975	35.2	175	I57667	activin receptor -
22	789.5	28.5	557	I50429	transforming growt
23	779	28.1	592	S51371	transforming growt
24	777.5	28.1	567	JN0459	transforming growt
25	775.5	28.0	592	A42100	transforming growt
26	775.5	28.0	1038	I38935	bone morphogenetic
27	774.5	28.0	567	A44225	transforming growt
28	770.5	27.8	1038	JC5527	bone morphogenetic
29	763.5	27.6	478	JC5373	transforming growt

RESULT 1
JQ1486
activin receptor II precursor - human
N:Contains: serine/threonine-specific protein kinase (EC 2.7.1.1.-)
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1992 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: JQ1486; S18908; S22345
R:Donaldson, C.J.; Mathews, L.S.; Vale, W.W.
Biochem. Biophys. Res. Commun. 184, 310-316, 1992
A:Title: Molecular cloning and binding properties of the human type II activin recept
A:Reference number: JQ1486; MUID:92231944; PMID:13114589
A:Accession: JQ1486
A:Molecule type: mRNA
A:Residues: 1-513 <DON>
A:CROSS-references: GB:M93415; NID:g178049; PIDN:AAA35504.1; PID:g178050
A:Experimental source: testis
R:Geisler, A.G.
submitted to the EMBL Data Library, December 1991
A:Reference number: S18908
A:Accession: S18908
A:Molecule type: mRNA
A:Residues: 1-513 <GEI>
A:CROSS-references: EMBL:X62381; NID:g28347; PIDN:CAA44245.1; PID:g28348
A:Experimental source: mammary gland epithelial cell line B5-589
R:Matzuk, M.M.; Bradley, A.
Biochim. Biophys. Acta 1130, 105-108, 1992
A:Title: Cloning of the human activin receptor cDNA reveals high evolutionary conserv
A:Reference number: S22345; MUID:92182002; PMID:1311955
A:Accession: S22345
A:Molecule type: mRNA
A:Residues: 1-513 <MAT2>
A:CROSS-references: EMBL:X63128; NID:g3928172; PIDN:CAA44839.1; PID:g28350
C:Comment: This protein binds activin A.
C:Genetics:
A:Gene: GDB:ACVR2
A:CROSS-references: GDB:132411
A:Map position: liq13-liq13
C:Superfamily: activin receptor II; protein kinase homology
C:Keywords: ATP; glycoprotein; phosphotransferase; receptor; serine/threonine-specifi
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-513/Product: activin receptor II #status predicted <EXT>
F:20-138/Domain: extracellular #status predicted <MAT>
F:139-160/Domain: transmembrane #status predicted <TML>
F:161-513/Domain: intracellular #status predicted <INT>
F:190-486/Domain: protein kinase homology <SKIN>
F:199-206/Region: protein kinase ATP-binding motif
F:43,66/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:219/Active site: Lys #status predicted

Query Match 99.9%; Score 2767; DB 1; Length 513;
Best Local Similarity 99.8%; Pred. No. 9.4e-142;
Matches 512; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 Db 1 MGAALAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 QY 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120
 Db 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120
 QY 121 EVTQPTSNVTPKPPYYNILLYSLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
 Db 121 EVTQPTSNVTPKPPYYNILLYSLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
 QY 181 PPPSPLLGLKPLQLLEVKGARFGCVKQAQLLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240
 Db 181 PPPSPLLGLKPLQLLEVKGARFGCVKQAQLLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240
 QY 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYVSNOLCHIAETMARGL 300
 Db 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYVSNOLCHIAETMARGL 300
 QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGQV 360
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGQV 360
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVEYMLPFEIEIG 420
 Db 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVEYMLPFEIEIG 420
 QY 421 QHPSLEDMEQVHVHKKRPVLDYQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
 Db 421 QHPSLEDMEQVHVHKKRPVLDYQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
 QY 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513
 Db 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513

RESULT 2

A39896
 activin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 18-Jun-1999
 C:Accession: A39896
 R:Mathews, L.S.; Vale, W.W.
 Cell 65, 973-982, 1991
 A:Title: Expression cloning of an activin receptor, a predicted transmembrane serine kinase
 A:Reference number: A39896; MUID:91256317; PMID:1646080
 A:Accession: A39896
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-513 <MAT>
 A:Cross-references: GB:M65287; NID:g191663; PIDN:AAA3171.1; PID:g191664
 C:Superfamily: activin receptor II; protein kinase homology
 C:Keywords: ATP; receptor; serine/threonine-specific protein kinase; transmembrane protein
 F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.7%; Score 2763; DB 2; Length 513;
 Best Local Similarity 99.4%; Pred. No. 1.5e-141;
 Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 Db 1 MGAALAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 QY 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120
 Db 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCEGNCNEKFSYFPEM 120
 QY 121 EVTQPTSNVTPKPPYYNILLYSLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
 Db 121 EVTQPTSNVTPKPPYYNILLYSLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180

QY 181 PPPSPLLGLKPLQLLEVKGARFGCVKQAQLLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240
 Db 181 PPPSPLLGLKPLQLLEVKGARFGCVKQAQLLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240
 QY 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYVSNOLCHIAETMARGL 300
 Db 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYVSNOLCHIAETMARGL 300
 QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGQV 360
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGQV 360
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVEYMLPFEIEIG 420
 Db 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVEYMLPFEIEIG 420
 QY 421 QHPSLEDMEQVHVHKKRPVLDYQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
 Db 421 QHPSLEDMEQVHVHKKRPVLDYQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
 QY 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513
 Db 481 QMORLTNIITTEDIVVTMTNVDPPKESL 513

RESULT 3

S27258
 activin receptor type II - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
 C:Accession: S27258
 R:Shinozaki, H.; Ito, I.; Hasegawa, Y.; Nakamura, K.; Igarashi, S.; Nakamura, M.; Miy
 FEBS Lett. 312, 53-56, 1992
 A:Title: Cloning and sequencing of a rat type II activin receptor.
 A:Reference number: S27258; MUID:93050162; PMID:1385212
 A:Accession: S27258
 A:Molecule type: mRNA
 A:Residues: 1-513 <SHI>
 A:Cross-references: GB:S48190; NID:g258941; PIDN:AAB23958.1; PID:g258942
 C:Superfamily: activin receptor II; protein kinase homology
 C:Keywords: ATP; receptor
 F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.7%; Score 2762; DB 2; Length 513;
 Best Local Similarity 99.2%; Pred. No. 1.7e-141;
 Matches 509; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 Db 1 MGAALAFVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 QY 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYFPEM 120
 Db 61 FATWKNISGSIEIVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCEGNCNEKFSYFPEM 120
 QY 121 EVTQPTSNVTPKPPYYNILLYSLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
 Db 121 EVTQPTSNVTPKPPYYNILLYSLVPLMLTAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
 QY 181 PPPSPLLGLKPLQLLEVKGARFGCVKQAQLLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240
 Db 181 PPPSPLLGLKPLQLLEVKGARFGCVKQAQLLNVEYVAVKIFPIQDKSQWNEYEYVSLPG 240
 QY 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYVSNOLCHIAETMARGL 300
 Db 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKANVYVSNOLCHIAETMARGL 300
 QY 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGQV 360
 Db 301 AYLEDIPGLKDGHPKPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGQV 360
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVEYMLPFEIEIG 420
 Db 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAADGPDVEYMLPFEIEIG 420

Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAAGDPVDEYMLPFEEIG 420
QY 421 QHPSLEDQEVVHHKKRPVLDYWKQKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
Db 421 QHPSLEDQEVVHHKKRPVLDYWKQKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVTVNDVPPPKSSSL 513
Db 481 QMORLTNIITTEDIVVTVMVTVNDVPPPKSSSL 513

RESULT 4

A49193
type II activin receptor ActRII - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
C:Accession: A49193
R:Eng, Z.M.; Madigan, M.B.; Chen, C.L.
Endocrinology 132, 2593-2600, 1993
A:Title: Expression of type II activin receptor genes in the male and female reproductiv
A:Reference number: A49193; MUID:93279247; PMID:7916681
A:Accession: A49193
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-513 <FEN>
A:Note: sequence extracted from NCBI backbone (NCBIN:133008, NCBI:133009)
C:Superfamily: activin receptor II; protein kinase homology
C:Keywords: ATP; receptor
F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.6%; Score 2759; DB 2; Length 513;
Best Local Similarity 99.2%; Pred. No. 2.5e-141;
Matches 509; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60
Db 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60
QY 61 FATWKNISGSIIEVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCEGNNCKEFSYFPEM 120
Db 61 FATWKNISGSIIEVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCEGNNCKEFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
Db 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
QY 181 PPPSLGLKPLQLLEVKARGFGCVKWAQLNEYVAVKIFPIQDKSQWNEYEYSLPG 240
Db 181 PPPSLGLKPLQLLEVKARGFGCVKWAQLNEYVAVKIFPIQDKSQWNEYEYSLPG 240
QY 241 MKHENILOFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300
Db 241 MKHENILOFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGKHPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Db 301 AYLEDIPGLKDGKHPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAAGDPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAAGDPVDEYMLPFEEIG 420
QY 421 QHPSLEDQEVVHHKKRPVLDYWKQKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
Db 421 QHPSLEDQEVVHHKKRPVLDYWKQKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVTVNDVPPPKSSSL 513
Db 481 QMORLTNIITTEDIVVTVMVTVNDVPPPKSSSL 513

RESULT 5

I45850

activin receptor type II - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: I45850
R:Ethier, J.F.; Houde, A.; Lussier, J.G.; Silversides, D.W.
Mol. Cell. Endocrinol. 106, 1-8, 1994
A:Title: Bovine activin receptor type II cDNA: cloning and tissue expression.
A:Reference number: I45850; MUID:95203477; PMID:7534730
A:Accession: I45850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-513 <ETH>
A:Cross-references: GB:L21717; NID:g393113; PIDN:AAA74597.1; PID:g393114
C:Genetics:
A:Gene: actRII
C:Superfamily: activin receptor II; protein kinase homology
C:Keywords: ATP; receptor
F:190-486/Domain: protein kinase homology <KIN>

Query Match 99.0%; Score 2743; DB 2; Length 513;
Best Local Similarity 98.4%; Pred. No. 1.8e-140;
Matches 505; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGAALKAFVAVFLISCGSAILGRSETQECLEFFNANWEKDRNTQGTVEPCYGDKKRRHC 60
Db 1 MGAALKAFVAVFLISCGSAILGRSETQECIFYNANWERDRTNRTGVESCYGDKKRRHC 60
QY 61 FATWKNISGSIIEVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCEGNNCKEFSYFPEM 120
Db 61 FATWKNISGSIIEVKQGCWLDLDINCYDRTDCIEKKDSPEVYFCCCEGNNCKEFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
Db 121 EVTQTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYRHHKMAYPVPLVPTQDPGP 180
QY 181 PPPSLGLKPLQLLEVKARGFGCVKWAQLNEYVAVKIFPIQDKSQWNEYEYSLPG 240
Db 181 PPPSLGLKPLQLLEVKARGFGCVKWAQLNEYVAVKIFPIQDKSQWNEYEYSLPG 240
QY 241 MKHENILOFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300
Db 241 MKHENILOFTGAERKGTSDVDLWLITAFHEKGSLSDFLKANYVSNWNLCHIAETMARGL 300
QY 301 AYLEDIPGLKDGKHPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Db 301 AYLEDIPGLKDGKHPAISHRDIKSKNVLKNNLTACIADFGALKEAGKSAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAAGDPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVLMELASRCTAAGDPVDEYMLPFEEIG 420
QY 421 QHPSLEDQEVVHHKKRPVLDYWKQKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
Db 421 QHPSLEDQEVVHHKKRPVLDYWKQKHAGMAMLCETIEECWDHDAEARSAGCVGERIT 480
QY 481 QMORLTNIITTEDIVVTVMVTVNDVPPPKSSSL 513
Db 481 QMORLTNIITTEDIVVTVMVTVNDVPPPKSSSL 513

RESULT 6

S23089
activin receptor type IIA - chicken
C:Species: Gallus gallus (chicken)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S23089
R:Ohuchi, H.; Noji, S.; Koyama, E.; Myokai, F.; Nishikawa, K.; Nohno, T.; Tashiro, K.
FEBS Lett. 303, 185-189, 1992
A:Title: Expression pattern of the activin receptor type IIA gene during differentiat
A:Reference number: S23089; MUID:92299088; PMID:1318847
A:Accession: S23089
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-513 <OHU>
 A:Cross-references: GB:D31899; NID:g505347; PIDN:BAA06697.1; PID:g505348
 C:Superfamily: activin receptor II; protein kinase homology
 C:Keywords: ATP
 F:190-486/Domain: protein kinase homology <KIN>

Query Match 94.0%; Score 2604; DB 2; Length 513;
 Best Local Similarity 92.2%; Pred. No. 5.4e-133;
 Matches 473; Conservative 26; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 DB 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 QY 61 FATWKNISGSIEIVKQGWCLDDINCYDRDTCVEKKDSPEYVFCCEGNCNEKSFYFPEM 120
 DB 61 FATWKNISGSIEIVKQGWCLDDINCYDRDTCVEKKDSPEYVFCCEGNCNEKSFYFPEM 120
 QY 121 EVTQPTSNPVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
 DB 121 EVTQPTSNPVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
 QY 181 PPPSPILGLKPLQLELVKARGFCGVKQAQLNEYVAVKFIPIQDKOSQWNEYEYISLPG 240
 DB 181 PPPSPILGLKPLQLELVKARGFCGVKQAQLNEYVAVKFIPIQDKOSQWNEYEYISLPG 240
 QY 241 MKHENILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNQLCHIAETMARGL 300
 DB 241 MKHENILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNQLCHIAETMARGL 300
 QY 301 AYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALAKFEAGKSAGDTHGOV 360
 DB 301 AYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALAKFEAGKSAGDTHGOV 360
 QY 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420
 DB 361 GTRRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEIG 420
 QY 421 QHPSLEDQEVVVHKKRPVLRDYQKSHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
 DB 421 QHPSLEDQEVVVHKKRPVLRDYQKSHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
 QY 481 QMQLTNIITTEDIVVTWTVNVDPPPKESSL 513
 DB 481 QMQLTNIITTEDIVVTWTVNVDPPPKESSL 513

RESULT 7

JQ1317
 activin receptor precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
 Accession: JQ1317
 R:Kondo, M.; Tashiro, K.; Fujii, G.; Asano, M.; Miyoshi, R.; Yamada, R.; Muramatsu, M.;
 Biochem. Biophys. Res. Commun. 181, 684-690, 1991
 A:Title: Activin receptor mRNA is expressed early in Xenopus embryogenesis and the level
 A:Reference number: JQ1317; MUID:92095974; PMID:1661587
 A:Accession: JQ1317
 A:Molecule type: mRNA
 A:Residues: 1-514 <KON>
 A:Cross-references: GB:S70930; NID:g240781; PIDN:AAB20638.1; PID:g240782
 C:Superfamily: activin receptor II; protein kinase homology
 C:Keywords: ATP; glycoprotein; serine/threonine-specific protein kinase; transmembrane
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-514/Product: activin receptor #status predicted <ACT>
 F:137-162/Domain: transmembrane #status predicted <TRA>
 F:191-487/Domain: protein kinase homology <KIN>
 F:46,67,88,214,334/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 89.6%; Score 2482.5; DB 2; Length 514;
 Best Local Similarity 87.7%; Pred. No. 1.8e-126;
 Matches 451; Conservative 37; Mismatches 25; Indels 1; Gaps 1;

QY 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 59
 DB 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 QY 60 CFATWKNISGSIEIVKQGWCLDDINCYDRDTCVEKKDSPEYVFCCEGNCNEKSFYFPE 119
 DB 61 CFATWKNISGSIEIVKQGWCLDDINCYDRDTCVEKKDSPEYVFCCEGNCNEKSFYFPE 120
 QY 120 MEVTQPTSNPVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 179
 DB 121 MEVTQPTSNPVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
 QY 180 PPPSPILGLKPLQLELVKARGFCGVKQAQLNEYVAVKFIPIQDKOSQWNEYEYISLPG 239
 DB 181 PPPSPILGLKPLQLELVKARGFCGVKQAQLNEYVAVKFIPIQDKOSQWNEYEYISLPG 240
 QY 240 GMKHNILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNQLCHIAETMARG 299
 DB 241 GMKHNILQFIAEGRGTSVDVLDLITAFHEKGSLSDFLKANYVSNQLCHIAETMARG 300
 QY 300 LAYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALAKFEAGKSAGDTHGO 359
 DB 301 LSHLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALAKFEAGKSAGDTHGO 360
 QY 360 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEI 419
 DB 361 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEI 420
 QY 420 QHPSLEDQEVVVHKKRPVLRDYQKSHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
 DB 421 QHPSLEDQEVVVHKKRPVLRDYQKSHAGMAMLCETIEECWDHDAEARLSAGCVGERI 480
 QY 480 TQMRLTNIITTEDIVVTWTVNVDPPPKESSL 513
 DB 481 IQMQLTNIITTEDIVVTWTVNVDPPPKESSL 514

RESULT 8

S21171
 activin receptor STK9 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 28-Feb-1997
 Accession: S21171
 R:Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N.
 FEBS Lett. 303, 81-84, 1992
 A:Title: Multiple genes for Xenopus activin receptor expressed during early embryogen
 A:Reference number: S21171; MUID:92275088; PMID:1317302
 A:Accession: S21171
 A:Molecule type: mRNA
 A:Residues: 1-512 <NIS>
 C:Superfamily: activin receptor II; protein kinase homology
 C:Keywords: ATP
 F:189-485/Domain: protein kinase homology <KIN>

Query Match 89.3%; Score 2474.5; DB 2; Length 512;
 Best Local Similarity 86.9%; Pred. No. 4.8e-126;
 Matches 446; Conservative 37; Mismatches 29; Indels 1; Gaps 1;

QY 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 DB 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQGTGVEPCYGDKRRHC 60
 QY 61 FATWKNISGSIEIVKQGWCLDDINCYDRDTCVEKKDSPEYVFCCEGNCNEKSFYFPEM 120
 DB 61 FATWKNISGSIEIVKQGWCLDDINCYDRDTCVEKKDSPEYVFCCEGNCNEKSFYFPEM 120
 QY 121 EVTQPTSNPVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
 DB 121 EVTQPTSNPVTPKPPYYNILLISLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 179
 QY 181 PPPSPILGLKPLQLELVKARGFCGVKQAQLNEYVAVKFIPIQDKOSQWNEYEYISLPG 240
 DB 180 PPPSPILGLKPLQLELVKARGFCGVKQAQLNEYVAVKFIPIQDKOSQWNEYEYISLPG 239

Qy	121	EVTQPTSNPVTPPPYNNILLYSLVPLMLIAGIVICAFVYVRHHKMAYPVLPVPTQDQGP	180
Db	121	ETFDKPDQ---PSASVNNILYLSLLPVGLSMAALLAFAMRYHRKPPYGHVEI-NEDPGL	176
Qy	181	PPSPLLGLKPLQLLEYKARGREGCVYKAQLLNEYVAVKFIPTDQRQSQWNEYEYVSLPG	240
Db	177	PPSPVGLKPLQLLEIKARGREGCVYKARLLNEYVAVKFIPTDQRQSQWCEKEIFTTPG	236
Qy	241	MKHENILQFTCAEKRGTSDVDVLLWLTITAPHEKSLSDFLKANVYVSNWNLCHTAETWARGL	300
Db	237	MKHENLLEFTAABKRGNSLMEWLITAFHDKGSLTDYLGKNLVSNWNEILCHTETWARGL	296
Qy	301	AYLHEDIPGLK-DGKHPAISHRIDKSNVLLKNLKTACTADFGALFKFAGKSAGDTHQG	359
Db	297	AYLHEDYPRCKGEGHKPAIAHDFKSNVLLRNDLTATLADFLGAVRFEPGKPPGDTHQG	356
Qy	360	VGTBRYMAPEVLEGAINFORDAFLRITDMYANGVLVLELASRCTAAADGPVDVYMLPEEEI	419
Db	357	VGTBRYMAPEVLEGAINFQRDSFIRITDMYANGVLVLEIVSRCTAAADGPVDVYLLPEEEI	416
Qy	420	GQHSLESDMQEVVYHKKRFLRYDQWKHAGMAMLCETTEECWDHDAEARLSAGCVGERI	479
Db	417	GQHSLESDQEVVYHKKIRPVFQKDWHLKHPGLAOLCVTTEECWDHDAEARLSAGCVVEERI	476

Db 417

Qy 480 TOMORLTLNIITEDIVTVVMTNVNDPFPKESL 513
:|:: | ::: ||||| |||||
Db 477 SQIRKSANGTSDCLVSIVTSVTNVDLPPESSI 510

RESULT 10
A56926
activin receptor II STH3 precursor - African clawed frog
N:Alternate names: activin receptor 1
N:Contains: protein kinase STK3 (EC 2.7.1.-)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 08-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: A56926; S21234
R:Hemmati-Briavanlou, A.; Wright, D.A.; Melton, D.A.
Dev. Dyn. 194, 1-11, 1992
A:Title: Embryonic expression and functional analysis of a Xenopus activin receptor
A:Reference number: A56926; PMID:1384808
A:Accession: A56926
A:Molecule type: mRNA
A:Residues: 1-510 <HEM>
A:Cross-references: GB:S49438; NID:g260043; PIDN:AAB24192.1; PID:g260044
A:Experimental source: oocytes
A>Note: sequence extracted from NCBI backbone (NCBIN:118655, NCBIP:118656)
R:Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N.
FEBS Lett. 303, 81-84, 1992
A:Title: Multiple genes for Xenopus activin receptor expressed during early embryogenesis
A:Reference number: G21171; MUID:92275088; PMID:1317302

F;I-19/Domain: signal sequence #status predicted <SIG>
F;20-510/Product: activin receptor II #status predicted <MAT>

F:138-310/Domain: intracellular #status predicted <IN1>
F:186-483/Domain: protein kinase homology <KIN>

F;215/Active site: Lys #status predicted

Query Match 71.0%; Score 1965.5; DB 1; Length 510;
Best Local Similarity 67.3%; Pred. No. 1.le-98;

Matches	346;	Conservative	88;	Mismatches	75;	Indels	5;	Gaps	3;
---------	------	--------------	-----	------------	-----	--------	----	------	----

[illegible]

```

RESULT 11
I37134
activin type II receptor - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C:Accession: I37134
R:Hilden, K.; Tuuri, T.; Eramaa, M.; Ritvos, O.
Blood 83, 2163-2170, 1994
A:Title: Expression of type II activin receptor genes during differentiation
A:Reference number: I37134; MUID:94214127; PMID:8161782
A:Accession: I37134
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
Residues: 1-512 <RES>
Cross-references: EMBL:X77533; NID:9825619; PIDN:CAA54671.1; PID:g825620
Superfamily: activin receptor II; protein kinase homology
F:188-485/Domain: protein kinase homology <KIN>

```

[illegible][illegible]

A:Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate

A:Reference number: A40829; MUID:92119722; PMID:1310075

A:Accession: C40829

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-528 <ATT>

A:Experimental source: Balb/c 3T3

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:88362, NCBIIP:88363)

C:Superfamily: activin receptor II; protein kinase homology

C:Keywords: Atp; receptor

F:204-501/Domain: protein kinase homology <KIN>

Query Match 69.4%; Score 1922; DB 2; Length 528;

Best Local Similarity 64.6%; Pred. No. 2.4e-96;

Matches 343; Conservative 87; Mismatches 67; Indels 34; Gaps 4;

Qy 8 AFAYFLISCSGAILGRSETOECLEFFNANWEKDRNTQNGVEPCYGDKDKRRHCFATWKN I 67

Db 7 ALALLWSLCAGSGRGEARETCIYYNANWELENTQSGLERCEGEQDKRLHCYASWRNS 66

Qy 68 SGSEIVKQGCWLDDINCYDRTDCVEKKDSPEVYFCCEGNMCNEKFSYPPEMEVTOPTS 127

Db 67 SGTIELVKGCWLDDINCYDRTDCVEKKDSPEVYFCCEGNMCNEKFSYPPEMEVTOPTS 118

Qy 128 NPVTPK-PPYNNILYSVLPLMLIAGIVICAFVWYRHKKMAYPPVLV----- 173

Db 119 -PGGPEAPTLLTLVLAISLLPIGGLSLVLLAFWMYRHRKPPYGHVDIHEVRQCORWAGRR 177

Qy 174 -----PTQDPGPPPPSPILGLKPLQLLEVKARGFCGVWKAQLLNEYVAVKIFPI 223

Db 178 DGCADSFKPLFPDQPPPPSPILGLKPLQLLEVKARGFCGVWKAQLLNEYVAVKIFPI 237

Qy 224 QDKQSWQNEYEVYSLPGMKHENILQFCAEKRGTSVDVLDLITAFHEKGSLSDFLKANV 283

Db 238 QDKQSWQSEREIFSTPGMKHENILQFCAEKRGTSVDVLDLITAFHEKGSLSDFLKANV 297

Qy 284 VSWNOLCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSKNVLKNNLTACIADF 342

Db 298 ITWNELCVHAETMSRGLSYLHEDVPWCRGEGKPSIAHROFCKSNVLLKSLDTAVLADF 357

Qy 343 LALKEACKSAGDTHGQVGTTRYWAPVLEGAIFNFORDAFLRIDMYAMGLVWELASRCT 402

Db 358 LAVREPKPGDTHGQVGTTRYWAPVLEGAIFNFORDAFLRIDMYAMGLVWELASRCT 417

Qy 403 AADGPVDEYMLPFEEIEIGHPSELDQEVVYVKKRPVLRDYQWKHAGMAMLCETIEECW 462

Db 418 AADGPVDEYMLPFEEIEIGHPSELDQEVVYVKKRPVLRDYQWKHAGMAMLCETIEECW 477

Qy 463 DHDAEARLSAGCVGRITQMORLNIITTEDIVTWVTWVTNVPFPPKESL 513

Db 478 DHDAEARLSAGCVGRITQMORLNIITTEDIVTWVTWVTNVPFPPKESL 528

Search completed: May 10, 2003, 18:00:11

Job time : 23 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 18:00:15 ; Search time 91 Seconds
(without alignments)
1161.562 Million cell updates/sec

Title: US-09-742-684A-16
Perfect score: 2770
Sequence: 1 MGAARKLAFAPFLISCSGA.....IVTVMTVMTVDPPKESL 513

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2616	94.4	513	13 Q90669	Q90669 gallus gall
2	2604	94.0	513	13 Q90745	Q90745 gallus gall
3	2474.5	89.3	512	13 Q9PSM0	Q9PSM0 xenopus lae
4	2001	72.2	512	13 Q90670	Q90670 gallus gall
5	1975.5	71.3	510	13 Q9PSL8	Q9PSL8 xenopus lae
6	1971.5	71.2	510	13 Q9PSL9	Q9PSL9 xenopus lae
7	1965.5	71.0	510	13 Q91962	Q91962 xenopus lae
8	1872.5	67.6	509	13 Q9YGU4	Q9YGU4 brachydanio
9	1824	65.8	504	13 Q13102	Q13102 carassius a
10	1500	54.2	292	13 Q9PSG1	Q9PSG1 gallus gall
11	1312.5	47.4	365	13 Q91347	Q91347 xenopus lae
12	1312.5	47.4	386	13 Q9PSL7	Q9PSL7 xenopus lae
13	1150.5	41.5	516	5 Q24468	Q24468 drosophila
14	1147.5	41.4	516	5 Q24229	Q24229 drosophila
15	1071	38.7	254	6 P79233	P79233 papio hamad
16	1034.5	37.3	233	13 Q9PSG2	Q9PSG2 gallus gall

17	996	36.0	262	6 Q95L45	Q95L45 ovis aries
18	975	35.2	175	11 Q64209	Q64209 rattus sp.
19	913	33.0	175	6 Q9GLC1	Q9GLC1 sus scrofa
20	886	32.0	159	6 Q95JA7	Q95JA7 oryctolagus
21	882.5	31.9	284	5 Q95T01	Q95T01 drosophila
22	789.5	28.5	557	13 Q90999	Q90999 gallus gall
23	779	28.1	567	11 Q91288	Q91288 mus musculus
24	775.5	28.0	530	4 Q13161	Q13161 homo sapien
25	774.5	28.0	567	6 Q9TS29	Q9TS29 mustela sp.
26	749.5	27.1	1048	13 P79954	P79954 xenopus lae
27	748	27.0	1031	13 Q42124	Q42124 gallus gall
28	733	26.5	534	13 Q9DE31	Q9DE31 xenopus lae
29	706.5	25.5	903	5 Q9NGX8	Q9NGX8 drosophila
30	703.5	25.4	903	5 Q95V83	Q95V83 drosophila
31	703.5	25.4	903	5 Q9VZ19	Q9VZ19 drosophila
32	664	24.0	532	11 Q64308	Q64308 rattus norv
33	662.5	23.9	527	13 Q42338	Q42338 xenopus lae
34	662.5	23.9	527	13 Q91578	Q91578 xenopus lae
35	656.5	23.7	533	13 Q9PUF5	Q9PUF5 coturnix co
36	656.5	23.7	533	13 Q90754	Q90754 gallus gall
37	655.5	23.7	527	13 Q42339	Q42339 xenopus lae
38	653.5	23.6	502	6 Q9BD14	Q9BD14 ovis aries
39	653.5	23.6	502	11 Q9QVT7	Q9QVT7 rattus sp.
40	651.5	23.5	502	6 Q95L23	Q95L23 sus scrofa
41	650	23.5	974	5 Q9UAG0	Q9UAG0 ephydaria f
42	640	23.1	530	13 Q9W629	Q9W629 brachydanio
43	639.5	23.1	493	4 Q8TBG2	Q8TBG2 homo sapien
44	638	23.0	500	13 Q91595	Q91595 xenopus lae
45	637.5	23.0	493	11 P70539	P70539 rattus norv

ALIGNMENTS

RESULT 1

Q90669 ID Q90669 PRELIMINARY; PRT; 513 AA.
AC Q90669;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Activin receptor IIA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069914; PubMed=7589799;
RA Stern C.D., Yu R.T., Kakizuka A., Kintner C.R., Mathews L.S.,
RA Vale W.W., Evans R.M., Umesono K.;
RT "Activin and its receptors during gastrulation and the later phases of
RT mesoderm development in the chick embryo.";
RL Dev. Biol. 172:192-205(1995).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31222; AAA87841.1;
DR HSSP; P27038; IRTS.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVINZR.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
KW ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 513 AA; 58092 MW; 03128AB7FF732552 CRC64;

Query Match 94.4%; Score 2616; DB 13; Length 513;
Best Local Similarity 92.4%; Pred. No. 7.1e-236;

```
Matches 474; Conservative 28; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MGAATKLAFAVELISCSSGAILGRSETQCELFNANWEKDRNTQGTGVEPCYGDKRRHC 60
Db 1 MGAATKLAFAVELISCSSGAILGRSETQCEIYYNANWEKDKTNRSGIEPCYGDKRRHC 60
Qy 61 FATWKNISGSIIEVKQGCWLDNDINCYDRTDCVKKDSPEVYFCCCEGNMCKNEFSYFPEM 120
Db 61 FATWKNISGSIIEVKQGCWLDNDINCYDNDCEIEKDSPEVYFCCCEGNMCKNERFSYFPEM 120
Qy 121 EVTQPTSNPVTPKPPYNYLLSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
Db 121 EVTQPTSNPVTPKPPYNYLLSLVPLMLIAGIVILFSEWYRHHKLAYPPVLPVPTQDGP 180
Qy 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKOSWONEVEYISLPG 240
Db 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKOSWONEVEYISLPG 240
Qy 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
Db 241 MKHDNILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNELCHIAQTMRGL 300
Qy 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Db 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Qy 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTAADGPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTASDGPVDEYMLPFEEIG 420
Qy 421 QHPSLDMQEVVYVHKRPVLRDYWQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
Db 421 QHPSLDMQEVVYVHKRPVLRDYWQKHAGMAMLCETIEECWDHDAEARLSAGCVGERII 480
Qy 481 QMOKLTNIITTEDIVTVVMTNVDVFPKESL 513
Db 481 QMOKLTNIITTEDIVTVVMTNVDVFPKESL 513
RESULT 2
Q90745 PRELIMINARY; PRT; 513 AA.
AC Q90745;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Activin receptor, type IIA.
GN ACTIVIN RECEPTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
MEDLINE=92299088; PubMed=1318847;
RA Chuchi H., Noji S., Koyama E., Miyokai F., Nishikawa K., Nohno T.,
RA Tashiro K., Shiohara K., Matsuo N., Taniguchi S.;
RT "Expression pattern of the activin receptor type IIA gene during
RT differentiation of chick neural tissues, muscle and skin.";
RL FEBS Lett. 303:185-189(1992).
[2]
SEQUENCE FROM N.A.
RA Nohno T.;
RA "None.";
RT Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D31899; BAA06697.1; -.
DR HSSP: P27038; 1BTE.
DR InterPro: IPR000472; Activin_rec.
DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kinase.
```

```
DR Pfam: PF01064; Activin_rec; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00653; ACTIVIN2R.
DR PRODOM: PD00001; Euk_pkinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 513 AA; 57923 MW; EIB4B8A026C41B80 CRC64;
Query Match 94.0%; Score 2604; DB 13; Length 513;
Best Local Similarity 92.2%; Pred. No. 9.4e-235;
Matches 473; Conservative 26; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MGAATKLAFAVELISCSSGAILGRSETQCELFNANWEKDRNTQGTGVEPCYGDKRRHC 60
Db 1 MGAATKLAFAVELISCSSGAILGRSETQCEIYYNANWEKDKTNRSGIEPCYGDKRRHC 60
Qy 61 FATWKNISGSIIEVKQGCWLDNDINCYDRTDCVKKDSPEVYFCCCEGNMCKNEFSYFPEM 120
Db 61 FATWKNISGSIIEVKQGCWLDNDINCYDNDCEIEKDSPEVYFCCCEGNMCKNERFSYFPEM 120
Qy 121 EVTQPTSNPVTPKPPYNYLLSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDGP 180
Db 121 EVTQPTSNPVTPKPPYNYLLSLVPLMLIAGIVILFSEWYRHHKLAYPPVLPVPTQDGP 180
Qy 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKOSWONEVEYISLPG 240
Db 181 PPPSLGLKPLQLLEVKARGFCVWKAQLNEYVAVKIFPIQDKOSWONEVEYISLPG 240
Qy 241 MKHENILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNOLCHIAETMARGL 300
Db 241 MKHDNILQFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNELCHIAQTMRGL 300
Qy 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Db 301 AYLEDIPGLKDGHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSAGDTHGOV 360
Qy 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTAADGPVDEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDMYAGLVWELASRCTASDGPVDEYMLPFEEIG 420
Qy 421 QHPSLDMQEVVYVHKRPVLRDYWQKHAGMAMLCETIEECWDHDAEARLSAGCVGERIT 480
Db 421 QHPSLDMQEVVYVHKRPVLRDYWQKHAGMAMLCETIEECWDHDAEARLSAGCVGERII 480
Qy 481 QMOKLTNIITTEDIVTVVMTNVDVFPKESL 513
Db 481 QMOKLTNIITTEDIVTVVMTNVDVFPKESL 513
RESULT 3
Q9PSM0 PRELIMINARY; PRT; 512 AA.
AC Q9PSM0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE XSf9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RA Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT "Multiple genes for Xenopus activin receptor expressed during early
RT embryogenesis.";
RL FEBS Lett. 303:81-84(1992).
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSSP: P27038; 1BTE.
DR InterPro: IPR000472; Activin_rec.
```

```

DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF01064; Activin_rec.1.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00653; ACTIVIN2R.
DR PRINTS: PR00653; ACTIVIN2R.
DR PRODOM: PD000001; Euk_pkinase.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 512 AA; 57819 MW; B784BD1B52D506F3 CRC64;

Query Match      89.3%; Score 2474.5; DB 13; Length 512;
Best Local Similarity 86.9%; Pred. No. 1.2e-222;
Matches 446; Conservative 37; Mismatches 29; Indels 1; Gaps 1;

QY 1 MGAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQTVGPECYGDKRRHCF 60
DB 1 MGAATKLAFAVFLISCSGAILGRLETKECIYYNANWEKDKTNSNGTEPCYGDNRKHC 60

QY 61 FATWKNISGSTEIVKQCGWLDINCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 120
DB 61 FATWKNISGSTEIVKQCGWLDINCYNKNEIEKESPDVFFCCCEGNCNERFYHSP 120

QY 121 EVTQPTNSPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHKKMAYPPVLVPTQDGP 180
DB 121 EVTQPTNSPVTPKPPLENTLLSLVPIIVAVILFVWYRHKKLGYPPELVPTQDGP 179

QY 181 PPSPLGLPLQLLEVKARGFCVWKAQLNEYVAVKFIPIQDKOSQWNEYEVYSLPG 240
DB 181 PPSPLGLPLQLLEVKARGFCVWKAQLNEYVAVKFIPIQDKOSQWNEYEVYSLPG 239

QY 241 MKHENILQFIAEKGRTSVDDVLLWLTAPHEKSLDFELKANVSVNQLCHTAETMARG 300
DB 241 MKHENILHFGIAEKGRTNLDLWLTTFHEKSLDFELKANVSVNQLCHTAETMARG 299

QY 301 AYLEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSGADTHGV 360
DB 301 SYLHEDIPGLKDGHPKPAVAHRDIKSNVLLKNNLTACIADFGALKEAGKSGADTHGV 359

QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETG 420
DB 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETG 419

QY 421 QHPSLDMQEVVHKRRPVLDYWKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 480
DB 420 QHPSLDMQEVVHKRRPVLDYWKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 479

QY 481 QMOKRLNIITTEDIVTVMTVNTVNDPPPKESL 513
DB 480 QMOKRLNIITTEDIVTVMTVNTVNDPPPKESL 512

RESULT 4
Q90670 ID Q90670 PRELIMINARY; PRT; 512 AA.
AC Q90670;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Activin receptor IIB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069914; PubMed=7589799;
RA Stern C.D., Yu R.T., Kakizuka A., Kintner C.R., Mathews L.S.,
RA Vale W.W., Evans R.M., Umesono K.;

```

```

RT "Activin and its receptors during gastrulation and the later phases of
RT mesoderm development in the chick embryo.";
RL Dev. Biol. 172:192-205(1995).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U31223; AAA87842.1; -.
DR HSP: P27038; 1BTE.
DR InterPro: IPR000472; Activin_rec.
DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF01064; Activin_rec.1.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00653; ACTIVIN2R.
DR PRODOM: PD000001; Euk_pkinase.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Receptor; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 512 AA; 57776 MW; 6051FOCB9E4AE060 CRC64;

Query Match      72.2%; Score 2001; DB 13; Length 512;
Best Local Similarity 68.9%; Pred. No. 2.4e-178;
Matches 353; Conservative 80; Mismatches 77; Indels 2; Gaps 2;

QY 3 AAATKLAFAVFLISCSGAILGRSETQECLEFFNANWEKDRNTQTVGPECYGDKRRHCF 62
DB 2 SASWLTAVLCATLGAGPGHGAETRECIYYNANWEKLEKTSQGVCEGEKDKRLHCA 61

QY 63 TWKNISGSTEIVKQCGWLDINCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 122
DB 62 SWRNSGSTEIVKQCGWLDINCYDRTDCVEKKDSPEYVFCCEGNCNEKFSYFPEM 121

QY 123 TQPTNSPVTPKPPYNYLLISLVPLMLIAGIVICAFWYRHKKMAYPPVLVPTQDGP 182
DB 122 PEVIYEPPPTPSLLNLIIVLSLPTAVLSVAILLAFWYRHKKPYGHVDI-NEDPGPP 180

QY 183 PPSPLGLPLQLLEVKARGFCVWKAQLNEYVAVKFIPIQDKOSQWNEYEVYSLPGM 242
DB 181 PPSPLGLPLQLLEVKARGFCVWKAQLMNDYVAVKFIPIQDKOSQWSEIEFNTPGM 240

QY 243 HENILQFIAEKGRTSVDDVLLWLTAPHEKSLDFELKANVSVNQLCHTAETMARG 302
DB 241 HENILQFIAEKGRTNLETLWLTAFHDKGSLDYLKGNISWNECHVATMARGLSY 300

QY 303 LHEDIPGLK-DGHPKPAISHRDIKSNVLLKNNLTACIADFGALKEAGKSGADTHGV 361
DB 301 LHEDVPWCKGEGHPKPAIAHRDFKSNVLLKNNLTAVLADFGLVAFEPKPGDTHGV 360

QY 362 TRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETG 421
DB 361 TRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAADGPVDEYMLPFEETG 420

QY 422 HPSLEDMEQEVVHKRRPVLDYWKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 481
DB 421 HPSLEDMEQEVVHKRRPVLDYWKQKAGMAMLCETIEECWHDHDAEARLSAGCVGERIT 480

QY 482 QMOKRLNIITTEDIVTVMTVNTVNDPPPKESL 513
DB 481 IRKSVNGTSDCLSVISVTNVDLPKESL 512

RESULT 5
Q9PSL8 ID Q9PSL8 PRELIMINARY; PRT; 510 AA.
AC Q9PSL8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE XSTK3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

```

```

RN RP SEQUENCE FROM N.A.
RX MEDLINE-92275088; PubMed=1317302;
RA Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT "Multiple genes for Xenopus activin receptor expressed during early
RT embryogenesis.";
RL FEBS Lett. 303:81-84(1992).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSSP; P27038; 18TE.
DR InterPro; IPR000472; Actin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 510 AA; 57852 MW; 3CD03B6A48953067 CRC64;

Query Match 71.3%; Score 1975.5; DB 13; Length 510;
Best Local Similarity 67.5%; Pred. No. 5.8e-176;
Matches 347; Conservative 89; Mismatches 73; Indels 5; Gaps 3;

QY 1 MGAATAAFVAVFLVSCSGAILGRSETQCLFFNANWEKDRTNQGTGVCYGDKRRHC 60
DB 1 MGAAVPLTALLAATFRAGSGHDEVEITRECIYNNANWELEKTNQSGVCEGDKRLHC 60
QY 61 FATKNISGSIEIVKQGCWLDINCYDRTDCVEKKDPSVEYFCCCEGNCNEKFSYFPEM 120
DB 61 YASWRNNSGFIELVKGWLDNFCYDQECIAKEENPVQVFFCCCEGNCNKKFTHLPEV 120
QY 121 EYVQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAPVPLVPTQDPGP 180
DB 121 ETFDPKPQM---PSVLNLIYSLPLIAGLSWVILLAFWYRHRKPPYGHVDL-NEDPGP 176
QY 181 PPSPLGLKPLQLLEVKARGFCGVKKAQLLNEVAVKIFPIODKQSWONEYEYSLPG 240
DB 177 TPSPVWGLKPLQLLEIKARGFCGVKARLLNEVAVKIFPVQDKQSWOCEKEIFNTPG 236
QY 241 MKHENILQFAGKRGTSVDVLDLWLTAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300
DB 237 MKHENLLEFIAEKRGSLNEMELWLITAFHDKGSLTDYLGKLVNWNELCHITETMARGL 296
QY 301 AYLEDIPGLK-DGHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 359
DB 297 SYLHEDVPRCKGEGHKAIAHRDFKSNVLRNDLTAILADFGLAVERPEKPPGDTHGQ 356
QY 360 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEI 419
DB 357 VGTTRYMAPEVLEGAINFQDSFLRDMYAMGLVWLWELVSVSCTAAGDPVDEYMLPFEEI 416
QY 420 GQHPSLDMQEVVYVHKRPVLDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
DB 417 GQHPSLDLQEVVYVHKRPVFKDHLKHPGLAQLCVITIEECWDHDAEARLSAGCVGERI 476
QY 480 TQMRLTNIITTEDIVTVVTVNVDPPKESL 513
DB 477 SQIRKSVNGTSDCLVSIIVTSVTVNDLPPKESI 510

RESULT 6
Q9PSL9 PRELIMINARY; PRT; 510 AA.
AC Q9PSL9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE xSTR8.
```

```

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92275088; PubMed=1317302;
RA Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT "Multiple genes for Xenopus activin receptor expressed during early
RT embryogenesis.";
RL FEBS Lett. 303:81-84(1992).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSSP; P27038; 18TE.
DR InterPro; IPR000472; Actin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 510 AA; 57782 MW; 99C7567C19F29992 CRC64;

Query Match 71.2%; Score 1971.5; DB 13; Length 510;
Best Local Similarity 67.9%; Pred. No. 1.4e-175;
Matches 349; Conservative 85; Mismatches 75; Indels 5; Gaps 3;

QY 1 MGAATAAFVAVFLVSCSGAILGRSETQCLFFNANWEKDRTNQGTGVCYGDKRRHC 60
DB 1 MGAVALTFLLLATFRAGSGHDEVEITRECIYNNANWELEKTNQSGVCEGDKRLHC 60
QY 61 FATKNISGSIEIVKQGCWLDINCYDRTDCVEKKDPSVEYFCCCEGNCNEKFSYFPEM 120
DB 61 YASWRNNSGFIELVKGWLDNFCYDQECIAKEENPVQVFFCCCEGNCNKKFTHLPEV 120
QY 121 EYVQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMAPVPLVPTQDPGP 180
DB 121 ETFDPKPQ---PSASVLNLIYSLPLVGLSMAILLAFWYRHRKPPYGHVEI-NEDPGL 176
QY 181 PPSPLGLKPLQLLEVKARGFCGVKKAQLLNEVAVKIFPIODKQSWONEYEYSLPG 240
DB 177 PPSPLVGLKPLQLLEIKARGFCGVKKAQLLNEVAVKIFPVQDKQSWOCEKEIFNTPG 236
QY 241 MKHENILQFAGKRGTSVDVLDLWLTAFHEKGSLSDFLKANYVSWNOLCHIAETMARGL 300
DB 237 MKHENLLEFIAEKRGSLNEMELWLITAFHDKGSLTDYLGKLVNWNELCHITETMARGL 296
QY 301 AYLEDIPGLK-DGHPAISHRDIKSNVLLKNNLTACIADFGALKFEAGKSAGDTHGQ 359
DB 297 AYLEDVPRCKGEGHKAIAHRDFKSNVLRNDLTAILADFGLAVERPEKPPGDTHGQ 356
QY 360 VGTTRYMAPEVLEGAINFORDAFLRDMYAMGLVWLWELASRCTAAGDPVDEYMLPFEEI 419
DB 357 VGTTRYMAPEVLEGAINFQDSFLRDMYAMGLVWLWELVSVSCTAAGDPVDEYMLPFEEI 416
QY 420 GQHPSLDMQEVVYVHKRPVLDYQWKHAGMAMLCETIEECWDHDAEARLSAGCVGERI 479
DB 417 GQHPSLDLQEVVYVHKRPVFKDHLKHPGLAQLCVITIEECWDHDAEARLSAGCVGERI 476
QY 480 TQMRLTNIITTEDIVTVVTVNVDPPKESL 513
DB 477 SQIRKSVNGTSDCLVSIIVTSVTVNDLPPKESI 510

RESULT 7
Q91962 PRELIMINARY; PRT; 510 AA.
ID Q91962
AC Q91962;
DT 01-NOV-1996 (Tremblrel. 01, Created)
```


Db 420 PSLDQAVVHKRLPAFKDCWLKHSGLQCMETMECDWDHDAEARLSAGCQVERISOI 479

Qy 483 ORLNTLTEDIVTVMVTNVDPPKESL 513

Db 480 RVSS-STSDCLFSWYSLTNVDLPKESSI 509

RESULT 9

O13102

ID O13102 PRELIMINARY; PRT; 504 AA.

AC O13102;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Activin type IIB receptor precursor.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary.

MD MEDLINE=97424747; PubMed=9278860;

RT "Cloning and characterization of goldfish activin type IIB receptor."

RL J. Mol. Endocrinol. 19:47-57(1997).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AF001406; AAB58749.1;

DR HSPF; P27038; ISTE.

DR InterPro; IPR000472; Activin_rec.

DR InterPro; IPR000333; Actn_receptorII.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF01064; Activin_rec; 1.

DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR00653; ACTIVIN2R.

DR PRODOM; PD000001; Euk_pkinase; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Receptor; Serine/threonine-protein kinase; Signal;

KW TRANSFERASE.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 504 ACTIVIN TYPE IIB RECEPTOR.

SQ SEQUENCE 504 AA; 57215 MW; CCB779A07992338F1 CRC64;

Query Match 65.8%; Score 1824; DB 13; Length 504;

Best Local Similarity 64.6%; Pred. No. 8.5e-162;

Matches 329; Conservative 83; Mismatches 81; Indels 16; Gaps 5;

Qy 9 FAVFLICSSGAILGRSETQCLFFNANWEKDRNTQGTGVEPCYGDKKRRHCFATWKNIS 68

8 FALLIGTFSGASHAEVTHECLYFNINWEVEKTRNSGVERCEGEKDRSHCYASWRNS 67

Qy 69 GSIEVKGCGWLDINCVDYDKCKDSPEVYFCCCEGNCMEKESFYFFEMEVQPTSN 128

68 GSILVKGCGWLDINCVDYDKCKDSPEVYFCCCEGNCMEKESFYFFEMEVQPTSN 127

Db 129 PVTPPPPPYINILL----YSLVPLMLIAGIVICAFWYRHHKMYAPPVLPTQDPGPPPPS 184

122 PVLESPPSAPULLLIIVLYSLPLVTMLSMLLGLGFWMYRHRKPPYGHVDL-SEDPSPSPS 180

Qy 185 PLLGLKPLQLLEVARGRGFCGWAKQLLNEVAVKIPPIQDKSQWONEYEYVSLPGMKHE 244

181 PLLTLLQLLLEVARGRGFCGWAKQLLNEVAVKIPPIQDKSQWONEYERDMFSTPGMKHE 240

Qy 245 NTLQFQAEKRGTSVDVWLITLITAFHEKGSLSDFLKANVSWNOLCHIAETMARGLAYLH 304

241 NLRYIGAEKRGANLETFEFLWITEFHEKGSLSDFLKGNVSWNOLCHIAETMARGLAYLH 300

Qy 305 EDIPGLKDGHPAISHKIKSNVLLKNTLACIADFGALKFEAGKSAGDTHGQVGTTR 364

301 EDVP----RSKPAIAHRDKSRNLLKSDLSAVLGLDLAVRFEFGTPPGDTHGQVGTTR 356

Qy 365 YMAPEVLEGAINFORDAFRLRIDMYAMGLVLMELASRCTAADGPVDEYMLPFEETIGQHP 424

Db 357 YMAPEVLEGAINFORDAFRLRIDMYAMGLVLMELASRCTAADGPVDEYMLPFEETIGQHP 416

Qy 425 LEDMQEVVHKKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARLSAGCGERITQMOR 484

Db 417 LEDLQDAVYHKKMRPAFKDCWLKHSGLQCMETMECDWDHDAEARLSAGCGERISQRR 476

Qy 485 LFNILTTEDIVTVMVTNVDPPKESL 513

Db 477 LFS-ITTSOLLSTVSLTNVDLSPKESRI 504

RESULT 10

Q9PSG1

ID Q9PSG1 PRELIMINARY; PRT; 292 AA.

AC Q9PSG1;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Activin receptor type IIA, ARIIA (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94159615; PubMed=8115385;

RA Nohno T., Noji S., Koyama E., Myokai F., Ohuchi H., Nishikawa K.,

RA Sumitomo S., Taniguchi S., Saito T.;

RT "Expression patterns of the activin receptor IIA and IIB genes during chick limb development."

RL Prog. Clin. Biol. Res. 383:705-714(1993).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR InterPro; IPR000333; Actn_receptorII.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR00653; ACTIVIN2R.

DR PRODOM; PD000001; Euk_pkinase; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Serine/threonine-protein kinase; Transferase.

FT NON_TER 1 292

FT NON_TER 292 292

SQ SEQUENCE 292 AA; 33173 MW; 9486ABDD28A256A1 CRC64;

Query Match 54.2%; Score 1500; DB 13; Length 292;

Best Local Similarity 95.2%; Pred. No. 7.6e-132;

Matches 278; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Qy 194 LLEVKARGFGCVKQAQLLNEVAVKIPPIQDKSQWONEYEYVSLPGMKHENILOFICAE 253

1 LLEIKARGFGCVKQAQLLNEVAVKIPPIQDKSQWONEYEYVSLPGMKHNLLOFICAE 60

Db 254 KRCTSDVDLWLITAFHEKGSLSDFLKANVSWNOLCHIAETMARGLAYLHEDIFGLKDG 313

61 KRCTSDVDLWLITAFHEKGSLSDFLKANVSWNOLCHIAETMARGLAYLHEDIFGLKDG 120

Qy 314 HKPAISHRDIKSNVLLKNTLACIADFGALKFEAGKSAGDTHGQVGTTRRYMAPEVLEG 373

121 HKPAISHRDIKSNVLLKNTLACIADFGALKFEAGKSAGDTHGQVGTTRRYMAPEVLEG 180

Qy 374 AINFQDAFLRIDMYAMGLVLMELASRCTAADGPVDEYMLPFEETIGQHPSEDMQEVVV 433

181 AINFQDAFLRIDMYAMGLVLMELASRCTAADGPVDEYMLPFEETIGQHPSEDMQEVVV 240

Qy 434 HKKRPVLRDYQWKHAGMAMLCETIEECWDHDAEARLSAGCGERITQMOR 485

Db 241 HKKRPVLRQKQSGMAMLCETIEECWDHDAEARSAGCVBERIIOMQKL 292

RESULT 11

Q91347 PRELIMINARY; PRT; 365 AA.
AC Q91347;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Activin receptor.
GN XSK2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93050187; PubMed=1330691;
RA Nishimatsu S., Iwao M., Nagai T., Oda S., Suzuki A., Asashima M.,
RA Murakami K., Ueno N.;
RT "A carboxyl-terminal truncated version of the activin receptor
mediates activin signals in early xenopus embryos."
RT FEBS Lett. 312:169-173(1992).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; S47891; AAB24030.1; -.
DR HSSP; P27038; 1BTE.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Receptor; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 365 AA; 41401 MW; 36BF5C05E7CE616 CRC64;

Query Match 47.4%; Score 1312.5; DB 13; Length 365;
Best Local Similarity 62.5%; Pred. No. 3.7e-114;
Matches 227; Conservative 72; Mismatches 59; Indels 5; Gaps 3;

QY 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVCYGDKRRHC 60
Db 1 MGAAPLTLALLATFRAGSGHDEVETRECIYNNANWELEKTNQSGVSCGEKDKRLHC 60
QY 61 FATWKNISGIEIVKQGCWLDIDNCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
Db 61 YASWRNNSGFIELYKKGWLDIDNCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMYPPVLVPTQDPGP 180
Db 121 ETEDPKQPM---PSVLNLIYSLPIAGLSWVILLAFWYRHHKPPYGHVDL-NEDPGP 176
QY 181 PPSPLGLKPLQLLEKARGGCVKAKQALLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240
Db 177 SPSPVMGLKPLQLLEKARGGCVKAKQALLNEYVAVKIFPIQDKSQWNEYEYVSLPG 236
QY 241 MKHENILOFTGAEKRTSDVDVLDLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGL 300
Db 237 MKHENLLEFIAERKSGNLEMLWLTAFHDKGSLTDYLGKLVNWNELCHITETMARGL 296
QY 301 AYLHEDIPLGLK-DGHKPAISHRDTKSKNVLKNNLTACIADCLAKFEAGKSGADTHGQ 359
Db 297 SYLHEDVPRCKGEGHKAIAHRDFKSKNVLIRNDLTAILADFLAVRFPKPGPDTHGQ 356
QY 360 VGT 362
Db 357 VIT 359

RESULT 12

Q9PSL7 PRELIMINARY; PRT; 386 AA.
AC Q9PSL7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Activin RECEPTOR-CLONE XSTK2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92275088; PubMed=1317302;
RA Nishimatsu S., Oda S., Murakami K., Ueno N.;
RT "Multiple genes for Xenopus activin receptor expressed during early
embryogenesis."
RT FEBS Lett. 303:81-84(1992).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR HSSP; P27038; 1BTE.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 43719 MW; 559F3F51AE4419CC CRC64;

Query Match 47.4%; Score 1312.5; DB 13; Length 386;
Best Local Similarity 62.5%; Pred. No. 4e-114;
Matches 227; Conservative 72; Mismatches 59; Indels 5; Gaps 3;

QY 1 MGAARKLAFVFLISCSGAILGRSETQCLFFNANWEKDRNTQGTGVCYGDKRRHC 60
Db 22 MGAAPLTLALLATFRAGSGHDEVETRECIYNNANWELEKTNQSGVSCGEKDKRLHC 81
QY 61 FATWKNISGIEIVKQGCWLDIDNCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPEM 120
Db 82 YASWRNNSGFIELYKKGWLDIDNCYDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPEM 141
QY 121 EVTQTSNPVTPKPPYNNILYSLVPLMLIAGIVICAFWYRHHKMYPPVLVPTQDPGP 180
Db 142 ETEDPKQPM---PSVLNLIYSLPIAGLSWVILLAFWYRHHKPPYGHVDL-NEDPGP 197
QY 181 PPSPLGLKPLQLLEKARGGCVKAKQALLNEYVAVKIFPIQDKSQWNEYEYVSLPG 240
Db 198 SPSPVMGLKPLQLLEKARGGCVKAKQALLNEYVAVKIFPIQDKSQWNEYEYVSLPG 257
QY 241 MKHENILOFTGAEKRTSDVDVLDLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGL 300
Db 258 MKHENLLEFIAERKSGNLEMLWLTAFHDKGSLTDYLGKLVNWNELCHITETMARGL 317
QY 301 AYLHEDIPLGLK-DGHKPAISHRDTKSKNVLKNNLTACIADCLAKFEAGKSGADTHGQ 359
Db 318 SYLHEDVPRCKGEGHKAIAHRDFKSKNVLIRNDLTAILADFLAVRFPKPGPDTHGQ 377
QY 360 VGT 362
Db 378 VIT 380

RESULT 13

Q24468 PRELIMINARY; PRT; 516 AA.
ID Q24468
AC Q24468;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 PUT OR PUNT OR CG7904.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95211840; PubMed=7697719;
 RA Basler K.;
 RT "An absolute requirement for both the type II and type I receptors,
 RT punt and thick veins, for dpp signaling in vivo.";
 RL Cell 80:889-897(1995).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AE003705; AAF55079.1; -;
 DR EMBL: L38495; AAC1566.1; -;
 DR FlyBase: FBgn0003169; put.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_pkinase.
 DR Pfam: PF01064; Activin_rec; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 516 AA; 58648 MW; B3F754DC603EC5BC CRC64;

Query Match

41.5%; Score 1150.5; DB 5; Length 516;

Best Local Similarity 47.2%; Pred. No. 8.9e-99;
 Matches 249; Conservative 83; Mismatches 152; Indels 43; Gaps 17;
 QY 5 AKLAFAPVLCSSGAILGRSETQCLFFNANWEK--DRTNQ--TGVEPCYGDKRRHC 60
 DB 11 AQLTVCLLIGHGSLPGSHGIECEHFD---EKMCNTTOCEETRIECHKWEADKPPSC 67
 QY 61 FATW--KNISGSIEIVKOGCWLDDINCYDRDTCVKKDSPE--VYFCCCEGNMCKEFSY 116
 DB 68 YVLWSVNETTGILRIKMGCEFTDMHEC--NOTECVTSABEPQGNTHFCCKGRCSNOKY 126
 QY 117 FPE-----MEVTOPTSNPVPKPPYNYLLSLVPLMLIAGIVICAFWVYRHHKMA 167
 DB 127 IKSTTEATQVPKKTQGSNDLY---IYIGTSVFSV--LMWIVGM---GLLLIARRKQA 178
 QY 168 YPPVLVLPVTPQDPPPPPLGLKPLQLLEVKARGFCVWKAQLLNEYVAYKIFPIQDKQ 227
 DB 179 HFNE-IPTHEAIFITNSPILLSNRPIQLLEQKASRGFDVQWQAKLNQDQVAVKIFRMQKE 237
 QY 228 SWQNEYVYSLPGMKHENILOFIGAERKGTVD--VDMLITAFIEHKGSLSDFLKANVYSW 286
 DB 238 SWTTEHDIVKLPFRMRPNLLEFLGVKEH---MDKPEYWLISYQHNGSLCDYLKSHSTISW 294
 QY 287 NOLCHIAETMARGLAYLHEDIPGLK-DGHPAISHRDITKSNVLLKNLNTACIADFGAL 345
 DB 295 PELCRIAESMANGLAHLHEEIPASTDGLKFSIAHRDFKSNVLLKSLDTACIADFGLAM 354
 QY 346 KFEAGKSGADTHGQVGTTRYNAPEVLEGAINFQDFAFLRIDMAMGLVWELASRCTAAD 405
 DB 355 IFQPKPCGDTHGQVGTTRYNAPEVLEGAINFNRDAFLRIDVYACGLVLEWMSRCDFA- 413
 QY 406 GPVDEYMLPFEEICQHPLESDEMQEYVYHKKRPVLRDYWKQKHAGMAMLCETIECDWDHD 465
 DB 414 GPVGFEQLPFEEALGRPSLDEVQESVYVYMKLRLPRLLSNRAHPLGNVFCDTMECDWDHD 473
 QY 466 AEARLSAGCVGERITQMORLTNIITTEDIVTVMTVMTVDFPPKSS 512
 DB 474 AEARLSGCVMERFQALNKYPS-----TQLLIKNTNID-DAKEST 513
 RESULT 14
 Q24229 PRELIMINARY; PRT; 516 AA.
 AC Q24229;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Activin receptor.
 GN PUT OR CG7904.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94022397; PubMed=8415726;
 RA Childs S.R., Wrana J.L., Arora K., Attisano L., O'Connor M.B.,
 RA Massague J.;
 RT "Identification of a Drosophila activin receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:9475-9479(1993).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: L22176; AAA03579.1; -;
 DR FlyBase: FBgn0003169; put.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF01064; Activin_rec; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 516 AA; 58643 MW; 3C3B2DDC603EC5BB CRC64;

Query Match 41.4%; Score 1147.5; DB 5; Length 516;
Best Local Similarity 47.8%; Pred. No. 1.7e-98;
Matches 251; Conservative 83; Mismatches 144; Indels 47; Gaps 19;

QY 11 VFLISC---SSGAIL-GRSETOCELFNFANWEK--DRTNQ--TGVEPCVGDGDKRRHCF 62
DB 13 VTLVCCLGIGHGSLPGSHGIIIECEHFD---ERMCNTTQOCETREHCKMEADKFPYCIV 69
QY 63 TW--KNISGSEIVKOGCWLDDINCVDRTDCVEKKDSE--VYFCCCEGNMCMNEKFSYFP 118
DB 70 LMSVNETTGILRIKMKGCCTDMHEC--NOTECVTSAPROGNIHFCCCKGRCSNQNKYIK 128
QY 119 E-----MEVTOPTSPNVPKPPYNNILYSVLPLMIAGIYCAIFAWYVRRHMKMAYP 169
DB 129 SYTEATVQPKETQDGSNLIY---IYIGTSVFSV--LMVIVGM--GLLLYRRRKQAHF 180
QY 170 PVLVPTQDPGPPPPSLLGLKPLQLLEVKARGFCVWKAQLLNEYVAVKIPPIQDKQSW 229
DB 181 NE-IPTHEAEITNSPSSLLSNRPITQLLEOKASGRFGDVWQAKLNNOADVAVKIFRMQEKESW 239
QY 230 QNEYEYSLPGMKHENILOFIGAERKGTSDV--VDLWLITAFHEKESLSDFLKANVVSQ 288
DB 240 TTEHDIYKUPRRHPHNIIEFLGVERH--MDKPEYWLISITVOHNSGLCDYLKSHITSWPE 296
QY 289 LCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSKNVLLKNLTACIADFGALKF 347
DB 297 LCRIAESMANGLAHLHEEIPASKTDLKPSIAHRDFKSKNVLLKSDLTACIADFGALMIF 356
QY 348 EAGKSGDTHGOVGTTRYMAPEVLEGAINFORDAFLRIDMYAMGLVLMELASRCTAADGP 407
DB 357 QPGKPCGDFHGOVGTTRYMAPEVLEGAINFNDRDAFLRIDVYACGLVLMELASRCTA 415
QY 408 VDEYMLPREEETGQHPLEDMQEVVHVKKRPVLRDYQKQKAGMAMLCETIEECWDHDAE 467
DB 416 VGEFQLPFAELGRPSLDEVOESVVMKKLRPLLNSRAHPLGLNVFCDTMEECWDHDAE 475
QY 468 ARLSAGCGERITOMRLTNIITTEDIVTVMTNVDFFPPKES 512
DB 476 ARLSSCVNERFAQLNKYPS-----TQLLKNHTNID-DAKEST 513

RESULT 15

P79233 PRELIMINARY; PRT; 254 AA.
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAY-2002 (TRENBLrel. 20, Last annotation update)
DE Activin receptor-like kinase (Fragment).
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_taxid=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=97112402; PubMed=8954082;
RA Zhao Y., Silbajoris R., Young S.L.;
RT "Identification and developmental expression of two activin receptors
in baboon lung.";
RL Biochem. Biophys. Res. Commun. 229:50-57(1996).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U06421; AAB40074.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Receptor; Serine/threonine-protein kinase.
FT NON_TER 1
FT NON_TER 254 254
SQ SEQUENCE 254 AA; 29041 MW; 481912040C3DC7DA CRC64;

Query Match 38.7%; Score 1071; DB 6; Length 254;
Best Local Similarity 75.2%; Pred. No. 8.4e-92;
Matches 191; Conservative 38; Mismatches 21; Indels 4; Gaps 2;

QY 216 VAVKIFPIQDKQSMQNEVEYVSLPGMKHENILOFIGAERKGTSDVVDLWLITAFHEKESL 275
DB 1 VAVKIFPIQDKQSMQNEVEYVSLPGMKHENILOFIGAERKGTSDVVDLWLITAFHEKESL 60
QY 276 SDFLKANVVSQNLCHIAETMARGLAYLHEDIPGLK-DGHKPAISHRDIKSKNVLLKNL 334
DB 61 TDYLGKNIITWNECHVAETMSRGLSYLHVEVPWCRGEGHKPSIAHRDFKSKNVLLKSDL 120
QY 335 ---TACIADFGALKFEAGKSGDTHGOVGTTRYMAPEVLEGAINFORDAFLRIDVYAMG 391
DB 121 ILFTAVLADFGLAVERFPKPPGPDTHGOVGTTRYMAPEVLEGAINFORDAFLRIDVYAMG 180
QY 392 LVLWELASRCTAADGPVDEYMLPREEETGQHPLEDMQEVVHVKKRPVLRDYQKQKAGM 451
DB 181 LVLWELVSRSKAADGPVDEYMLPREEETGQHPLEDMQEVVHVKKRPVLRDYQKQKAGM 240
QY 452 AMLCETIEECWDHD 465
DB 241 AQLCVTIEECWDHD 254

Search completed: May 10, 2003, 18:08:47
Job time : 94 secs


```

DR EMBL; D31770; BAA06548.1; -.
DR PIR; S18908; S18908.
DR PIR; JQ1486; JQ1486.
DR PIR; S22345; S22345.
DR HSP; P27038; ISTE.
DR Genew; HGNC:173; ACVR2.
DR MM; 102581; -.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 513
FT DOMAIN 20 135
FT TRANSMEM 136 161
FT DOMAIN 162 513
FT NP_BIND 198 206
FT BINDING 219 219
FT ACT_SITE 322 322
FT CARBOHYD 43 43
FT CARBOHYD 66 66
FT CONFLICT 13 13
FT CONFLICT 204 206
FT CONFLICT 348 348
SQ SEQUENCE 513 AA; 57847 MW; A89822E880979618 CRC64;

Query Match 99.98; Score 2767; DB 1; Length 513;
Best Local Similarity 99.88; Pred. No. 2e-199;
Matches 512; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MGAAKLAFVFLSCSGAILGRSETQECLEFFNANNEKDRNTGTGVCYGDKRRHC 60
Db 1 MGAAKLAFVFLSCSGAILGRSETQECLEFFNANNEKDRNTGTGVCYGDKRRHC 60
Oy 61 FATWNISSGSIIEVKQGCWLDINDCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120
Db 61 FATWNISSGSIIEVKQGCWLDINDCYDRTDCVEKKDSPEVYFCCCEGNCNEKFSYPPEM 120
Oy 121 EYVQTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
Db 121 EYVQTSNPVTPKPPYYNLLYSLVPLMLIAGIVICAFWYRHHKMAYPVLPVPTQDPGP 180
Oy 181 PPPSLLGLKPLQLLEVKARGFCVCKAQLNLLNEVAVKIFPIQDKQSWQNEYEVYSLPG 240
Db 181 PPPSLLGLKPLQLLEVKARGFCVCKAQLNLLNEVAVKIFPIQDKQSWQNEYEVYSLPG 240
Oy 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNQCHIAETMARGL 300
Db 241 MKHENILOFIGAERKGTSDVDLMLITAFHEKGSLSDFLKNVYVSNQCHIAETMARGL 300
Oy 301 AYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACTADPGLALKEFAGKSAGDTHGOV 360
Db 301 AYLHEDIPGLKDGHPKPAISHRDIKSNVLLKNNLTACTADPGLALKEFAGKSAGDTHGOV 360
Oy 361 GTRRYMAPEVLEGAINFORDAFLRIDYAMGLVLWELASRCTAADGPDVEYMLPFEEIG 420
Db 361 GTRRYMAPEVLEGAINFORDAFLRIDYAMGLVLWELASRCTAADGPDVEYMLPFEEIG 420
Oy 421 QHPSLEDQEVVYVHKRPVLRDYNQKAGWAMLCETIEECWDHDAEARLSAGCVGRIT 480
Db 421 QHPSLEDQEVVYVHKRPVLRDYNQKAGWAMLCETIEECWDHDAEARLSAGCVGRIT 480
Oy 481 QMQLRTNIITTEDIVVTVMVTNVDPPKSSSL 513

```

```

Db 481 QMQLRTNIITTEDIVVTVMVTNVDPPKSSSL 513
RESULT 2
AVR2_MOUSE
ID AVR2_MOUSE STANDARD; PRT; 513 AA.
AC P27038;
DT 01-AUG-1992 (Rel. 23; Created)
DT 01-AUG-1992 (Rel. 23; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
GN ACVR2 OR ACVR2A.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91256317; PubMed=1646080;
RA Mathews L.S.; Vale W.W.;
RT "Expression cloning of an activin receptor, a predicted transmembrane
RL serine kinase.";
RL Cell 65:973-982(1991).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 25-121.
RX MEDLINE=99101377; PubMed=9886286;
RA Greenwald J., Fischer W.H., Vale W.W., Choe S.;
RT "Three-finger toxin fold for the extracellular ligand-binding domain
RT of the type II activin receptor serine kinase.";
RL Nat. Struct. Biol. 6:18-22(1999).
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC -!- INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN, TESTIS, INTESTINE, LIVER, AND KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
TGFB RECEPTOR SUBFAMILY.
-----
This SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; M65287; AAA37171.1; -.
DR PIR; A39896; A39896.
DR PDB; 1BTE; 09-FEB-99.
DR MGD; MGI:102806; Acvr2.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 513
FT DOMAIN 20 135
FT TRANSMEM 136 161
FT DOMAIN 162 513
FT NP_BIND 198 206
FT BINDING 219 219
FT ACT_SITE 322 322

```

```

FT CARBOHYD 43 43 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 513 AA; 57889 MW; 475CD292506BAC61 CRC64;

Query Match 99.7%; Score 2763; DB 1; Length 513;
Best Local Similarity 99.4%; Pred. No. 3.9e-199;
Matches 510; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDGDKRRHC 60
D 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDGDKRRHC 60
QY 61 FATWKNISGSIEIVKQGCWLDLINCVDYRDCVEKDSPEVYFCCCGNMCNEKESYFPEM 120
D 61 FATWKNISGSIEIVKQGCWLDLINCVDYRDCVEKDSPEVYFCCCGNMCNEKESYFPEM 120
QY 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
D 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
QY 181 PPPSPLLGKPLQLLEVKGARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYEVYSLPG 240
D 181 PPPSPLLGKPLQLLEVKGARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYEVYSLPG 240
QY 241 MKHENILQFTGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVSNWLNCHIAETMARGL 300
D 241 MKHENILQFTGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVSNWLNCHIAETMARGL 300
QY 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKAGDTHGOV 360
D 301 AYLHEDIPGLKDGKHPAISHRDIKSNVLLKNNLTACIADFGALKEAGKAGDTHGOV 360
QY 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCCTAAGDPVDEYMLPFEETG 420
D 361 GTRRYMAPEVLEGAINFQDAFLRIDMYAMGLVWELASRCCTAAGDPVDEYMLPFEETG 420
QY 421 QHPSLEDMQBVVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARSAGCGERIT 480
D 421 QHPSLEDMQBVVHKRPVLDYQKQKAGMAMLCETIEECWDHDAEARSAGCGERIT 480
QY 481 QMORLNIITTEDIVVTVMTVNDVPPKESL 513
D 481 QMORLNIITTEDIVVTVMTVNDVPPKESL 513

RESULT 3
AVR2_RAT
ID AVR2_RAT STANDARD; PRT; 513 AA.
AC P38444;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
GN ACVR2 OR ACTRII.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93279247; PubMed=7916681;
RX Feng Z.M., Madigan M.B., Chen C.L.C.;
RA "Expression of type II activin receptor genes in the male and female
RT reproductive tissues of the rat.";
RL Endocrinology 132:2593-2600(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=93050162; PubMed=1385212;
RX Shinozaki H., Ito I., Hasegawa Y., Nakamura K., Igarashi S.,
RA Nakamura M., Miyamoto K., Bto Y., Ibuki Y., Minegishi T.;
RT "Cloning and sequencing of a rat type II activin receptor.";
```

```

RL FEBS Lett. 312:53-56(1992).
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFβ RECEPTOR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; L10639; AAA40674.1; -;
DR EMBL; S48190; AAB23958.1; -;
DR HSSP; P27038; 1BTE.
DR InterPro; IPR000472; Activin_rec.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 513 ACTIVIN RECEPTOR TYPE II.
FT DOMAIN 20 135 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 136 161 POTENTIAL.
FT DOMAIN 162 513 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 192 485 PROTEIN KINASE.
FT NP_BIND 198 206 ATP (BY SIMILARITY).
FT BINDING 219 219 ATP (BY SIMILARITY).
FT ACT_SITE 322 322 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 165 165 M -> K (IN REF. 2).
FT CONFLICT 218 218 V -> I (IN REF. 2).
FT CONFLICT 353 353 G -> A (IN REF. 2).
FT CONFLICT 475 475 L -> V (IN REF. 2).
SQ SEQUENCE 513 AA; 57892 MW; CE3A8742EF91DD7D CRC64;

Query Match 99.3%; Score 2750; DB 1; Length 513;
Best Local Similarity 98.8%; Pred. No. 3.7e-198;
Matches 507; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDGDKRRHC 60
D 1 MGAALAFVFLISCGSAILGRSETQCLFFNANWEKDRNTQGTVEPCYGDGDKRRHC 60
QY 61 FATWKNISGSIEIVKQGCWLDLINCVDYRDCVEKDSPEVYFCCCGNMCNEKESYFPEM 120
D 61 FATWKNISGSIEIVKQGCWLDLINCVDYRDCVEKDSPEVYFCCCGNMCNEKESYFPEM 120
QY 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
D 121 EVTQPTSNPVTPKPPYNNILLYSLVPLMLIAGIVICAFWYVRHHKWAYPPVLVPTQDPGP 180
QY 181 PPPSPLLGKPLQLLEVKGARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYEVYSLPG 240
D 181 PPPSPLLGKPLQLLEVKGARGCGVWKAQLLNEYVAVKIFPIQDKOSQWNEYEVYSLPG 240
QY 241 MKHENILQFTGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVSNWLNCHIAETMARGL 300
D 241 MKHENILQFTGAEKRGTSVDVLDLITAFHEKGSLSDFLKVNVSNWLNCHIAETMARGL 300
```



```

OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Romey; TISSUE=Ovarian follicle;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RC Tisdall D.J.;
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; LI9442; AAA91903.1; -
CC HSSP; P27038; 1BTE.
CC InterPro; IPR000472; Activin_rec.
CC InterPro; IPR000333; Actn_receptorII.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF01064; Activin_rec; 1.
CC PRINTS; PR00653; ACTIVIN2R.
CC ProDom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 513 ACTIVIN RECEPTOR TYPE II.
FT DOMAIN 20 135 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 136 161 POTENTIAL.
FT DOMAIN 162 513 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 192 485 PROTEIN KINASE.
FT NP_BIND 198 206 ATP (BY SIMILARITY).
FT BINDING 219 219 ATP (BY SIMILARITY).
FT ACT_SITE 322 322 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 513 AA; 57768 MW; 7231BF9E85CA57E3 CRC64;

Query Match 97.6%; Score 2704; DB 1; Length 513;
Best Local Similarity 97.1%; Pred. No. 1e-194;
Matches 498; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTNOTGVEPCYGDOKRRHC 60
DB 1 MGAALAFVFLISCSGAILGRSETQCLFFNANWEKDRNTNOTGVEPCYGDOKRRHC 60

QY 61 FATWKNISGIEIVKOGCDDLDINCVDRTDCVEKDPSPVYFCCCGNMCNEKFSYFPEM 120
DB 61 FATWKNISGIEIVKOGCDDLDINCVDRTDCIEKDPSPVYFCCCGNMCNEKFSYFPEM 120

QY 121 EVTQPTSNVTPKPPYNNILSLVPLMLIAGIVICAFWYRHKKMAYPPVLVPTQDPGP 180
DB 121 EVTQPTSNVTPKPPYNNILSLVPLMLIAGIVICAFWYRHKKMAYPPVLVPTQDPGP 180

QY 181 PPSPLGLKPLQLLEVKARGGCGVWKAQLLNEYAVKFIQDKSQHONEYEYSLPG 240
DB 181 PPSPLGLKPLQLLEVKARGGCGVWKAQLLNEYAVKFIQDKSQHONEYEYSLPG 240

QY 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVSNOLCHIAETMARGL 300
DB 241 MKHENILQFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANVSNOLCHIAETMARGL 300

```

RESULT 6

AVR2_XENLA STANDARD; PRT; 514 AA.

```

AC P27039;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9205974; PubMed=1661587;
RA Kondo M., Tashiro K., Fujii G., Asano M., Miyoshi R., Yamada R.,
RA Muramatsu M., Shikawa K.;
RT "Activin receptor mRNA is expressed early in Xenopus embryogenesis
RT and the level of the expression affects the body axis formation.";
RL Biochem. Biophys. Res. Commun. 181:684-690(1991).
CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.

```

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

```

EMBL; S70930; AAB20638.1; -
PIR; JQ1317; JQ1317.
HSSP; P27038; 1BTE.
InterPro; IPR000472; Activin_rec.
InterPro; IPR000333; Actn_receptorII.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF01064; Activin_rec; 1.
PRINTS; PR00653; ACTIVIN2R.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
Receptor; Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 514 ACTIVIN RECEPTOR TYPE II.
FT DOMAIN 21 136 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 137 162 POTENTIAL.

```

FT	DOMAIN	163	514	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	193	486	PROTEIN KINASE.
FT	NP_BIND	199	207	ATP (BY SIMILARITY).
FT	BINDING	220	220	ATP (BY SIMILARITY).
FT	ACT_SITE	323	323	BY SIMILARITY.
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	67	67	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	514 AA;	57903 MW;	9FA4B4D7F9756C26 CRC64;
Query Match				
Best Local Similarity 89.6%; Score 2482.5; DB 1; Length 514;				
Matches 451; Conservative 37; Mismatches 25; Indels 1; Gaps 1;				
Qy	1	MGA	AAKAF	AVFLISCS - GAILRSETQCLFENANWEKDRNTQTVGPCYGDKKRRH 59
Db	1	MGA	ATKAF	AVFLISCSAGSILGRSETKECIYANANWEKDKTNSNGTEICYGDNKRRH 60
Qy	60	CFAT	WKNIS	GIETVKGCGWLDLINCVDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPE 119
Db	61	CFAT	WKNIS	GIETVKGCGWLDLINCYNKSKTEKKDSDPVFFCCCGNMCNEKFSYFPE 120
Qy	120	MEVT	QTSNP	VPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDPG 179
Db	121	MEVT	QTSNP	VPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDPG 180
Qy	180	PPPS	PLGLK	PLQLEVKARGFCVWKAQLLNEYAVKIFPIQDKQSWQNEYEYVSLP 239
Db	181	PPPS	PLGLK	PLQLEVKARGFCVWKAQLLNEYAVKIFPIQDKQSWQNEYEYVSLP 240
Qy	240	GMKH	ENILQ	FGAKRGTSVDVDLWLITAFHEKGSLSDFLKANNVSNQICHAEIMARG 299
Db	241	GMKH	ENILY	FGAKRGTSVDVDLWLITAFHEKGSLSDFLKANNVSNQICHAEIMARG 300
Qy	300	LAYL	HEDIP	GLKGKHPAISHRDIKSNVLLKNNLTACIADFGLALFEAGKSAGDTHGQ 359
Db	301	LSHL	HEDIP	GLKGKHPAISHRDIKSNVLLKNNLTACIADFGLALFEAGKSAGDTHGQ 360
Qy	360	VGTR	RYMA	PEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAAGDGVDEYMLPFEEI 419
Db	361	VGTR	RYMA	PEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAAGDGVDEYMLPFEEV 420
Qy	420	GQHS	LEDQ	EVVHKRPVLDYWKHAGMAMLCETIECDWDHDAEALSGACGVERI 479
Db	421	GQHS	LEDQ	EVVHKRPVLDYWKHAGMAMLCETIECDWDHDAEALSGACGVERI 480
Qy	480	TQMR	LNIIT	EDIVTV 513
Db	481	IQMK	LNIIT	EDIVTV 514
RESULT 7				
RB_XENLA				
AC	AVPB_XENLA	STANDARD;	PRT;	511 AA.
DT	01-AUG-1992	(Rel. 23, Created)		
DT	01-AUG-1992	(Rel. 23, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Activin receptor type IIB precursor (EC 2.7.1.37) (ACTR-IIB).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-92205349; PubMed-1313188;			
RA	Mathews L.S., Vale W.W., Kintner C.R.;			
RT	"Cloning of a second type of activin receptor and functional			
RL	characterization in xenopus embryos."			
RL	Science 255:1702-1705(1992).			
CC	-1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.			
CC	-1- INVOLVED IN TRANSMEMBRANE SIGNALING.			

CC	-1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	TGFB RECEPTOR SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; M88594; AB000480.1; -			
DR	HSSP; P27038; 1BTE.			
DR	InterPro; IPR000472; Activin_rec.			
DR	InterPro; IPR000333; Actn_receptorII.			
DR	InterPro; IPR000719; Euk_pkinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase..			
DR	Pfam; PF00069; pkinase; 1.			
DR	Pfam; PF01064; Activin_rec; 1.			
DR	PRINTS; PR00653; ACTIVIN2R.			
DR	ProDom; PD000001; Euk_pkinase; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
KW	Receptor; Transferrase; Serine/threonine-protein kinase; ATP-binding;			
FT	Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 511			
FT	DOMAIN 21 133			
FT	EXTRACELLULAR (POTENTIAL).			
FT	POTENTIAL.			
FT	TRANSMEM 134 159			
FT	DOMAIN 160 511			
FT	CYTOPLASMIC (POTENTIAL).			
FT	PROTEIN KINASE.			
FT	NP_BIND 195 203			
FT	ATP (BY SIMILARITY).			
FT	BINDING 216 216			
FT	ATP (BY SIMILARITY).			
FT	ACT_SITE 320 320			
FT	BY SIMILARITY.			
FT	CARBOHYD 43 43			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 67 67			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	SEQUENCE 511 AA; 57935 MW; A87F1E6BC78C92F0 CRC64;			
Qy	1	MGA	AAKAF	AVFLISCSGAILGRSETQCLFENANWEKDRNTQTVGPCY -GDKDKRRH 59
Db	1	MGA	SVALT	TELLLLATFRAGSGHDEVTRECIYANANWELEKTNQSGVERLVGKKDKRLH 60
Qy	60	CFAT	WKNIS	GIETVKGCGWLDLINCVDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPE 119
Db	61	CYAS	WRNNS	GFIELVKKCGWLDLINCVDRTDCVEKKDSPEVYFCCCGNMCNEKFSYFPE 120
Qy	120	MEVT	QTSNP	VPKPPYNNILYSLVPLMLTAGIVICAFWYRHHKWAYPPVLVPTQDPG 179
Db	121	VETFD	PKPQ	---PSASVNLILYSLLPVIGLSMAILAFWYRHHKPSYGVHVEI -NEDPG 176
Qy	180	PPPS	PLGLK	PLQLEVKARGFCVWKAQLLNEYAVKIFPIQDKQSWQNEYEYVSLP 239
Db	177	LPSP	PLVGL	KPLQLLDIKARGFCVWKAQLLNEYAVKIFPIQDKQSWQNEKEIFTPP 236
Qy	240	GMKH	ENILQ	FGAKRGTSVDVDLWLITAFHEKGSLSDFLKANNVSNQICHAEIMARG 299
Db	237	GMKH	ENILQ	FGAKRGTSVDVDLWLITAFHEKGSLSDFLKANNVSNQICHAEIMARG 296
Qy	300	LAYL	HEDIP	GLKGKHPAISHRDIKSNVLLKNNLTACIADFGLALFEAGKSAGDTHG 358
Db	297	LAYL	HEDIP	GLKGKHPAISHRDIKSNVLLKNNLTACIADFGLALFEAGKSAGDTHG 356
Qy	359	QVGT	RYMA	PEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAAGDGVDEYMLPFEE 418
Db	357	QVGT	RYMA	PEVLEGAINFQDAFLRIDMYAMGLVWELASRCTAAGDGVDEYMLPFEE 416

Query Match 70.3%; Score 1947; DB 1; Length 511;
Best Local Similarity 67.4%; Pred. No. 3.7e-138;
Matches 347; Conservative 86; Mismatches 76; Indels 6; Gaps 4;

```
QY 419 IGQHPSEDMQEVVVVHKKRPVLRDQWKHAGMAMLCETIEECWDHDAEARLSAGCVGER 478
Db 417 IGQHPSELDQEVVVVHKKRPVLFKQHLKGLAQQLCTIEECWDHDAEARLSAGCVER 476
QY 479 ITOMORLTNIITIEDIVVTWMTVNDVDFPKKESL 513
Db 477 ISQIRSVNGTSDCLVSVITVNTVDLPKKESS 511

RESULT 8
ID AVRB_HUMAN STANDARD; PRT; 512 AA.
AC Q13705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
FE Activin receptor type IIB precursor (EC 2.7.1.37) (ACTR-IIB).
GN ACVR2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94214127; PubMed=8161782;
RA Hilden K., Tuuri T., Eramaa M., Ritvos O.;
RT "Expression of type II activin receptor genes during differentiation
RT of human K562 cells and cDNA cloning of the human type IIB activin
RT receptor.";
RL Blood 83:2163-2170(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=98284539; PubMed=9621519;
RA Ishikawa S., Kai M., Murata Y., Tamari M., Daigo Y., Murano T.,
RA Ogawa M., Nakamura Y.;
RT "Genomic organization and mapping of the human activin receptor type
RT IIB (hActr-IIB) gene.";
RL J. Hum. Genet. 43:132-134(1998).
RN [3]
RN SEQUENCE FROM N.A.; ALTERNATIVE SPLICING, AND VARIANTS LR AXIS
RX MALFORMATIONS HIS-40 AND ILE-454.
RX MEDLINE=99113885; PubMed=9916847;
RA Kosaki R., Gebbia M., Kosaki K., Lewin M., Bowers P., Towbin J.A.,
RA Casey B.;
RT "Left-right axis malformations associated with mutations in ACVR2B,
RT the gene for human activin receptor type IIB.";
RL Am. J. Med. Genet. 82:70-76(1999).
CC -I- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B AND INHIBIN A.
CC INVOLVED IN TRANSMEMBRANE SIGNALING.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 isoforms: ACTR-IIB1 and ACTR-IIB2 (shown
CC here); may be produced by alternative splicing. ACTR-IIB1 results
CC from the insertion in the transcript of 82 base pairs, leading to
CC frameshift and protein truncation. It is not known whether or not
CC ACTR-IIB1 has any biological function.
CC -I- DISEASE: Defects in ACVR2B are a cause of left-right (LR) axis
CC malformations, due to the loss of normal left-right asymmetry.
CC Complete left-right asymmetry reversal imparts to deleterious
CC consequences to the affected individual, whereas randomization
CC typically results in complex, often lethal heart malformations as
CC well as abdominal abnormalities.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFB RECEPTOR SUBFAMILY.

-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```

```
CC EMBL: X77533; CRA54571.1; -
DR EMBL: AB008681; DAA24180.2; -
DR EMBL: AF060202; AAC64515.1; -
DR EMBL: AF060199; AAC64515.1; JOINED.
DR EMBL: AF060200; AAC64515.1; JOINED.
DR EMBL: AF060201; AAC64515.1; JOINED.
DR HSSP: P27038; 1BPE.
DR Genew: HGNC:174; ACVR2B.
DR MIM: 602730; -
DR InterPro: IPR000472; Activin_rec.
DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF01064; Activin_rec; 1.
DR PRINTS: PR00653; ACTIVIN2R.
DR ProDom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor; transferase; Serine/threonine-protein kinase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal; Disease mutation;
KW Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 512
FT DOMAIN 19 134
FT TRANSMEM 135 160
FT DOMAIN 161 512
FT DOMAIN 190 480
FT NP_BIND 196 204
FT BINDING 217 217
FT ACT_SITE 321 321
FT CARBOHYD 42 42
FT CARBOHYD 65 65
FT VARIANT 40 40
FT VARIANT 494 494
FT CONFLICT 16 17
FT CONFLICT 64 64
FT CONFLICT 459 459
FT CONFLICT 459 459
FT CONFLICT 459 459
SQ SEQUENCE 512 AA; 57638 MW; 13E3225073E229A3 CRC64;

Query Match 70.28; Score 1944; DB 1; Length 512;
Best Local Similarity 67.3%; Pred. No. 6.2e-138;
Matches 342; Conservative 88; Mismatches 76; Indels 2; Gaps 2;

QY 7 LAFAVFLISCSGAILGRSETQECLEFFNANWEKORTNOTGVEPCYGDKRRHCFATWKN 66
Db 6 VALALLWGLSCLAGSGRGAETRECIYNNANWELERTNOSGLERCEGQDRLHCHYASWAN 65
QY 67 IGSIEIVQGCWLDDINCYDRTDCVEKKSPYVYFCCCEGNCMCNEKSFYFPEMEVTPQT 126
Db 66 SSGTIELVKKGCWLDDNFCYDRECVATEENPQVYFCCCEGNCNEFTLHPEAGGEVT 125
QY 127 SNVPTPPPPYNNILSYSLVPLMLTAGLVICAFWYRHHKWAYPPVLYPTQDPGPPPSPL 186
Db 126 YEPPTPTLTUTVAYSLPLTGGUSLVLLAFWYRHKPPYGHVDI-HEDPGPPPSPL 184
QY 187 LGLQLQLLEKARGFGCVKWAQLLNEYVAVKIFPLQDKQSWONEYVYSLPMKHENI 246
Db 185 VGLKPLQLLEKARGFGCVKWAQLLMDFVAVKIFPLQDKQSWQSEIREIFSTPMKHENL 244
QY 247 LQFICAKRGTSVDVLDLWLTAFHEKSLSDFLKANVVSNNQLCHIAETWARGLAYLHED 306
Db 245 LQFIAEKRGSNLEVELWLITAFHDKSLFDYLNKNIITWNLCHVAETMSRGLSYLHED 304
QY 307 IPGLK-DGHPAISHRDITKSNVLLKNNLTACTADFGALKFEAGKSGAGTHQGVTRY 365
Db 305 VPCRGEGCHKPSTIAHRDFKSNVLLKSDLTAVLADFLAVRFPKPGPDTHQGVTRY 364
```


-!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ACTR-IIB1 (SHOWN HERE), ACTR-IIB2, ACTR-IIB3 AND ACTR-IIB4; ARE PRODUCED BY ALTERNATIVE SPLICING. ACTR-IIB1 AND ACTR-IIB2 HAVE SIMILAR BUT HIGHER AFFINITIES FOR ACTIVIN A THAN ACTR-II, ACTR-IIB3 AND ACTR-IIB4. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. TGF β RECEPTOR SUBFAMILY. ----- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). ----- EMBL: M84120; AAA37172.1; -. AVRB_RAT RESULT 11 HSP; P27038; IBTE. AVRB_RAT ID AVRB_RAT STANDARD; PRT; 382 AA. AC P38445; DT 01-OCT-1994 (Rel. 30, Created) DT 01-OCT-1994 (Rel. 30, Last sequence update) DE Activin receptor type IIB (EC 2.7.1.37) (ACTR-IIB* (Fragment)). GN ACVR2B OR ACTRIIB. OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. OX NCBI_TaxID=10116; RN [1] SEQUENCE FROM N.A. RC STRAIN=Sprague-Dawley; TISSUE=Testis; MEDLINE=93279247; PubMed=7916681; RA Feng Z.M., Madigan M.B., Chen C.L.C.; RT "Expression of type II activin receptor genes in the male and female reproductive tissues of the rat."; RL Endocrinology 132:2593-2600(1993). CC -!- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A. CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. CC -!- SUBCELLULAR LOCATION: Type I membrane protein. CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. TGF β RECEPTOR SUBFAMILY. ----- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). ----- EMBL: L10640; AAA0772.1; -. DR InterPro; IPR000719; Euk_pkinase. DR InterPro; IPR002290; Ser_thr_pkinase. DR Pfam; PF00069; pkinase; 1. DR ProDom; PD000001; Euk_pkinase; 1. DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG. DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG. DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1. KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding; Transmembrane; Glycoprotein. FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL). FT DOMAIN <1 19 POTENTIAL. FT TRANSMEM 20 46 CYTOPLASMIC (POTENTIAL). FT DOMAIN 47 382 PROTEIN KINASE. FT DOMAIN 76 366 ATP (BY SIMILARITY). FT NP_BIND 82 90 ATP (BY SIMILARITY). FT BINDING 103 103 ATP (BY SIMILARITY). FT ACT_SITE 207 207 BY SIMILARITY. FT NON_TER 382 382 SEQUENCE 382 AA; 42909 MW; E812FEF574B4A3E CRC64;

Query Match 69.8%; Score 1934; DB 1; Length 536; Best Local Similarity 64.7%; Pred. No. 3.7e-137; Matches 343; Conservative 87; Mismatches 76; Indels 24; Gaps 2; QY 8 AFVFLISCSGAILGRSETQGLFNFANVEKDRNTQTVGPECYGDKRRHCFATWKN 67 Db 7 ALLMWSLCSGGRGEAEATRECIYTYNANWELERTNQSGLERCEGQDKRLHCYASWRNS 66 QY 68 SGSEIIVKQCWLDDINCYDRTDCVEKKDSPEYVFCCEGNCNCRKFSYFPEMEVTQPTS 127 Db 67 SGRIELVKKCWLDDFNCYDRQCVATEENPQVYFCCGNGFNCFNRTHLPPEGGPEVY 126 QY 128 NPVTKPPYNYLLSYLVPLMLIAGIVICAFWYVYRHKKMAYPPVLY----- 173 Db 127 EPPPTAPTLLTVLAYSLLPIGGLSLIVLLAFWMYRHRKPPYGHVDIHEVRCQRMAGRDR 186 QY 174 -----PTQPGPPPSPLGLPLQLLEVKARGCGVWKAQLNEYVAVKIFPTQ 224 Db 187 GCADSFKPLFQDPGPPPSPLVGLPLQLLEIKARGFCGVWKAQLMDFVAVKIFPLQ 246 QY 225 DKQSWNEYVYSLPGMKHENILOFTCAEKGTSVDVDLWLTATFAHKGSLDFLKANVY 284 Db 247 DKQSWSEREIFTPGKMKHENILOFTAAEKGNSLEVEVLWLTATFAHKGSLDYLGKNI 306

```
Query Match 52.7%; Score 1460; DB 1; Length 382;
Best Local Similarity 68.9%; Pred. No. 6.4e-102;
Matches 264; Conservative 62; Mismatches 55; Indels 2; Gaps 2;

Qy 116 YPEMEVTPQTSNPVTPKPPYNTLLSLVPLMLIAGIVICAFWYRHHKMYPPVLPVPT 175
Db 1 HLPEPGGPEVYEPPTAPTLLTVLAYSLLPIGGLSLIVLLAFWYRHHKPPYGHVDI-H 59

Qy 176 QDPGPPPSPLGLKPLQLLEKARGRGFCVWKAQQLNVEYVAVKFIQDKSQWQNEVEV 235
Db 60 EDGPPPPSPLVGLKPLQLLEKARGRGFCVWKAQQLNDFVAVKFIQDKSQWQNEVEV 119

Qy 236 YSLPGMKHENTLQITGAERKGTSDVDLWLTITAPHEKGSLSDFLKANVSVNWLCHTAET 295
Db 120 FSTPGMKHENTLQITGAERKGTSDVDLWLTITAPHEKGSLSDFLKANVSVNWLCHTAET 179

Qy 296 MARGLAYLHEDIPLGL-DGHPALSHRDIKSNVLLKNNLTACIADFGALKPEAGKSAG 354
Db 180 MSRGSLYLHEDVPMCRGEGHAKPSIAHREKSKNVLLKSDLTAVLADFGAVRFEPPGPG 239

Qy 355 DTHGOVGRTRYMAPEVLEGAINFORDAFLRIDMYAMGLVWLWELASRCAADGPVDEYMLP 414
Db 240 DTHGOVGRTRYMAPEVLEGAINFORDAFLRIDMYAMGLVWLWELASRCAADGPVDEYMLP 299

Qy 415 FEEIGOHPSLEDQEVVYVHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARSAGC 474
Db 300 SEEIGOHPSLEELQEVVYVHKKRPVLRDYWKHAGMAMLCETIEECWDHDAEARSAGC 359

Qy 475 VGERITOMRTNITTEDIVTV 497
Db 360 VEVRSLIRSVNGSTSDCLVSL 382

RESULT 12
TGR2_MOUSE STANDARD; PRF; 592 AA.
AC Q62312; Q63947;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TGF-beta receptor type II precursor (EC 2.7.1.37) (TGR-2) (TGF-beta
DE type II receptor).
GN TGFBR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
MEDLINE=95046367; PubMed=7957954;
SU Suzuki A., Shioda N., Maeda T., Tada M., Ueno N.;
RT "Cloning of an isoform of mouse TGF-beta type II receptor gene.";
RL FEBS Lett. 355:19-22(1994).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=94163970; PubMed=8119124;
RA Lawler S., Candia A.F., Ebner R., Shum L., Lopez A.R., Moses H.L.,
RA Wright C.V., Derynck R.;
RT "The murine type II TGF-beta receptor has a coincident embryonic
RT expression and binding preference for TGF-beta 1.";
RL Development 120:165-175(1994).
CC -1- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
CC COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC SIGNAL TRANSDUCERS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; RII-1 AND RII-2 (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT. EXPRESSED PRIMARILY
CC IN MESENCHYME AND EPIDERMIS OF THE MIDGESTATIONAL FETUS.
CC -1- PTM: PHOSPHORYLATED ON A SER/THR RESIDUE IN THE CYTOPLASMIC
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92154690; PubMed=1310899;
 RA Lin H.Y., Wang X.-F., Ng-Eaton E., Weinberg R.A., Lodish H.F.;
 RT "Expression cloning of the TGF-beta type II receptor, a functional
 transmembrane serine/threonine kinase."; <http://www.lsb-sib.ch/announce/>
 RL Cell 68:775-785(1992).
 RN [2]
 RP ERRATUM.
 RA Lin H.Y., Wang X.-F., Ng-Eaton E., Weinberg R.A., Lodish H.F.;
 RL Cell 70:1068-1068(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96411693; PubMed=8812462;
 RA Takenoshita S., Hagiwara K., Nagashima M., Gemma A., Bennett W.P.,
 RA Harris C.C.;
 RT "The genomic structure of the gene encoding the human transforming
 growth factor beta type II receptor (TGF-beta.RII).";
 RL Genomics 36:341-344(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96438608; PubMed=8840968;
 RA Lu S.-L., Zhang W.C., Akiyama Y., Nomizu T., Yuasa Y.;
 RT "Genomic structure of the transforming growth factor beta type II
 receptor gene and its mutations in hereditary nonpolyposis colorectal
 cancers.";
 RL Cancer Res. 56:4595-4598(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97128789; PubMed=8973329;
 RA Ogasa H., Noma T., Murata H., Kawai S., Nakazawa A.;
 RT "Cloning of a cDNA encoding the human transforming growth factor-beta
 type II receptor: heterogeneity of the mRNA.";
 RL Gene 181:185-190(1996).
 RN [6]
 RP VARIANT HNPCC MET-315.
 RX MEDLINE=98250164; PubMed=9590282;
 RA Lu S.-L., Kawabata M., Imamura T., Akiyama Y., Nomizu T., Miyazono K.,
 RA Yuasa Y.;
 RT "HNPCC associated with germline mutation in the TGF-beta type II
 receptor gene."; <http://www.lsb-sib.ch/announce/>
 RL Nat. Genet. 19:17-18(1998).
 CC -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
 COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
 SIGNAL TRANSDUCERS.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: PHOSPHORYLATED ON A SER/THR RESIDUE IN THE CYTOPLASMIC
 DOMAIN.
 CC -!- DISEASE: DEFECTS IN TGFBR2 ARE THE CAUSE OF HEREDITARY
 NONPOLYPOSI COLONRECTAL CANCER (HNPCC).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF RECEPTOR SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.lsb-sib.ch/announce/>
 or send an email to license@lsb-sib.ch).
 CC -----
 DR EMBL; M85079; AAB1164.1; -;
 DR EMBL; U52246; AAB17553.1; -;
 DR EMBL; U52240; AAB17553.1; JOINED.
 DR EMBL; U52241; AAB17553.1; JOINED.
 DR EMBL; U52242; AAB17553.1; JOINED.
 DR EMBL; U52244; AAB17553.1; JOINED.

DR EMBL; U52245; AAB17553.1; JOINED.
 DR EMBL; U69152; AAB40916.1; -;
 DR EMBL; U69146; AAB40916.1; JOINED.
 DR EMBL; U69147; AAB40916.1; JOINED.
 DR EMBL; U69148; AAB40916.1; JOINED.
 DR EMBL; U69149; AAB40916.1; JOINED.
 DR EMBL; U69150; AAB40916.1; JOINED.
 DR EMBL; U69151; AAB40916.1; JOINED.
 DR EMBL; D50683; BAA09332.1; -;
 DR PIR; A42100; A42100.
 DR Genew; HGNC:11773; TGFBR2.
 DR MIM; 190182; -;
 DR InterPro; IPR000472; Activin_rec.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Phosphorylation; Glycoprotein; Signal;
 KW Disease mutation.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 567 TGF-BETA RECEPTOR TYPE II.
 FT DOMAIN 167 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 167 187 POTENTIAL.
 FT DOMAIN 188 567 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 244 544 PROTEIN KINASE.
 FT NP_BIND 250 258 ATP (BY SIMILARITY).
 FT BINDING 277 277 ATP (BY SIMILARITY).
 FT ACT_SITE 379 379 BY SIMILARITY.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 315 315 T -> M (IN HNPCC).
 FT CONFLICT 381 381 /FTID=VAR_008156.
 FT SEQUENCE 567 AA; 64539 MW; C8DAC3651FFBC4FB CRC64;
 SQ
 Query Match 28.0%; Score 775.5; DB 1; Length 567;
 Best Local Similarity 35.6%; Pred. No. 1.4e-50;
 Matches 176; Conservative 82; Mismatches 140; Indels 97; Gaps 15;
 QY 60 CFATWNKSGSIEIVKGGWLDINDYD-----ETVCHDPKLPYHDFILEDAAAPKIMKEKKPGTFFM 135
 DB 84 CVAVWRKNDENITL-----ETVCHDPKLPYHDFILEDAAAPKIMKEKKPGTFFM 135
 QY 103 CCCEGNMCNEKFSYFPFEMEVTQPTSNPTKPPYYNLL-----YSLVPLMLIAGIVI 155
 DB 136 CSCSDECDNIIIFSEYN-----TSNP-----DLLLVIFQVTGISLPLGLVAISVI 183
 QY 156 CAFWYVRHHKMAPPPVLPVTPQDPGPPPP-----SPLLG 188
 DB 184 IIFYCYRVNRQ---QKLSSTWETGTRKLMFESEHCAILEDSDRSISSTCANNHNTE 240
 QY 189 LKPLQLLEVKARGFGCVKQAQLN-----EYVAVKIFPIQDKQWQNEVEYVSLPGMK 242
 DB 241 LLPIELDTLVKGRAEYVKAKLKQNTSEQFETVAVKIFPEYEAWSKTEKIDFSDINK 300
 QY 243 HENILOFIGAEKRGTSVDVLDLITAFHEKGSLSDFLKANYVSNOLCHIAETMARGLAY 302
 DB 301 HENILOFLTAERKTELGKQYWLITAFHAKGNLQYELTRHVISWEDRLKGLSGLANGIAH 360
 QY 303 LHEDIPLGDKGHKPA-----ISHRDIKSNVLLKNNLTACIADFGLALKFEAGSAGD- 355
 DB 361 LHSD-----HTPCGPRKMPIVHRDLKSNLILVKNLTCCLCDFGLSLRLOPTLSVDL 413
 QY 356 -THQGVQTRRYMAPEVLEGAINPQR-DAFLRIDMYAMGLVLMELASRCRTAAGPVDVEYML 413
 DB 414 ANSGQVGTARYMAPEVLESRMLENAESPKQTDVYSMALVLMELTSCNNAV-GEVKDYEP 472
 QY 414 PFEEIIGQHPLESMDQEVVVVHKKRPVLDYQKQKHAGMAMLCETIECDHDAEARLSAG 473

```

Db 473 PFSGKREHPCVSMKDNVLRGRPEIPSWLNHQIGMVCEITLTCWDHDPPEARLTAQ 532
QY 474 CVGERITOMORLTNI 488
Db 533 CVAERSELEHLRL 547

RESULT 15
BMR2_HUMAN
ID BMR2_HUMAN STANDARD; PRT; 1038 AA.
AC Q13873; Q16569;
DC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein receptor type II precursor (EC 2.7.1.37)
DE Bone morphogenetic protein receptor type II precursor (EC 2.7.1.37)
DE (BMP type II receptor) (BMPR-II).
DE BMR2 OR PPH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Substantia nigra;
RX MEDLINE=95372334; PubMed=7644468;
RA Rosenzweig B.L., Imamura T., Okadome T., Cox G.N., Yamashita H.,
RA ten Dijke P., Heldin C., Miyazono K.;
RT "Cloning and characterization of a human type II receptor for bone
RT morphogenetic proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7632-7636(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin fibroblast;
RX MEDLINE=95403457; PubMed=7673243;
RA Nohno T., Ishikawa T., Saito T., Hosokawa K., Noji S., Wosing D.H.,
RA Rosenbaum J.S.;
RT "Identification of a human type II receptor for bone morphogenetic
RT protein-4 that forms differential heteromeric complexes with bone
RT morphogenetic protein type I receptors.";
RL J. Biol. Chem. 270:22522-22526(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95197572; PubMed=7890683;
RA Kawabata M., Chytil A., Moses H.L.;
RT "Cloning of a novel type II serine/threonine kinase receptor through
RT interaction with the type I transforming growth factor-beta
RT receptor.";
RL J. Biol. Chem. 270:5625-5630(1995).
RN [4]
RP VARIANTS PPH GLN-491 AND TRP-491.
RX PubMed=10903931;
RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,
RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.E.,
RA Knowles J.A.;
RT "Familial primary pulmonary hypertension (gene PPH1) is caused by
RT mutations in the bone morphogenetic protein receptor-II gene.";
RL Am. J. Hum. Genet. 67:737-744(2000).
RN [5]
RP VARIANTS PPH TYR-60; TYR-117 AND ARG-483.
RX PubMed=11015450;
RA Thomson J.R., Machado R.D., Paucululo M.W., Morgan N.V., Humbert M.,
RA Elliott G.C., Ward K., Yacoub M., Mikhail G., Rogers P., Newman J.H.,
RA Wheeler L., Higenbottam T., Gibbs J.S.R., Egan J., Crozier A.,
RA Peacock A., Allcock R., Corris P., Loyd J.E., Trembath R.C.,
RA Nichols W.C.;
RT "Sporadic primary pulmonary hypertension is associated with germline
RT mutations of the gene encoding BMPR-II, a receptor member of the
RT TGF-beta family.";
RL J. Med. Genet. 37:741-745(2000).
RN [6]
RP VARIANTS PPH TRP-118; TYR-347 AND GLY-485.
RX PubMed=10973254;

```

```

RA Lane K.B., Machado R.D., Paucululo M.W., Thomson J.R., Aldred M.,
RA Phillips J.A. III, Loyd J.E., Nichols W.C., Trembath R.C., Gaddipati R.,
RA Brannon C.A., Conneally P.M., Foroud T., Fretwell N., Gaddipati R.,
RA Koller D., Loyd E.J., Morgan N.V., Newman J.H., Prince M.A.,
RA Villarino Gueell C., Wheeler L.;
RT "Heterozygous germline mutations in BMPR2, encoding a TGF-beta
RT receptor, cause familial primary pulmonary hypertension.";
RL Nat. Genet. 26:81-84(2000).
RN [7]
RP VARIANTS PPH ARG-123; SER-123; ARG-420 AND THR-512, VARIANT ASP-224,
RP AND CHARACTERIZATION OF VARIANT PPH GLY-485.
RX PubMed=11115378;
RA Machado R.D., Paucululo M.W., Thomson J.R., Lane K.B., Morgan N.V.,
RA Wheeler L., Phillips J.A. III, Newman J.H., Williams D., Galie N.,
RA Manes A., McNeil K., Yacoub M., Mikhail G., Rogers P., Corris P.,
RA Humbert M., Donnai D., Martensson G., Tranebjaerg L., Loyd J.E.,
RA Trembath R.C., Nichols W.C.;
RT "BMPR2 haploinsufficiency as the inherited molecular mechanism for
RT primary pulmonary hypertension.";
RL Am. J. Hum. Genet. 68:92-102(2001).
CC -!- FUNCTION: BINDS TO BMP-7, BMP-2 AND, LESS EFFICIENTLY, BMP-4.
CC BINDING IS WEAK BUT ENHANCED BY THE PRESENCE OF TYPE I RECEPTORS
CC FOR BMPs.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: HETERODIMERIZE WITH TYPE-I RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND LIVER.
CC -!- DISEASE: Defects in BMPR2 are the cause of primary pulmonary
CC hypertension (PPH), a rare autosomal dominant disorder
CC characterized by pleomorphic lesions of proliferating endothelial
CC cells in pulmonary arterioles. The lesions lead to elevated
CC pulmonary arterial pressure, right ventricular failure, and death.
CC The disease can occur from infancy throughout life and it has a
CC mean age at onset of 36 years. Penetrance is reduced. Although
CC familial PPH is rare, cases secondary to known etiologies are more
CC common and include those associated with the appetite-suppressant
CC drugs.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC TGFb RECEPTOR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z48923; CAA88759.1; -.
CC EMBL; D50516; BAA09094.1; -.
CC EMBL; U20165; AAC50105.1; -.
CC Genew; HGNC:1078; BMPR2.
CC MIM; 600799; -.
CC MIM; 178600; -.
CC InterPro; IPR000472; Activin_rec.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF01064; Activin_rec; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
CC Transmembrane; Glycoprotein; Signal; Polymorphism; Disease mutation.
CC SIGNAL 1 26
CC CHAIN 27 1038 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE
CC II.
CC DOMAIN 27 150 EXTRACELLULAR (POTENTIAL).
CC TRANSEM 151 171 POTENTIAL.
CC DOMAIN 172 1038 CYTOPLASMIC (POTENTIAL);
CC DOMAIN 203 504 PROTEIN KINASE.
CC NP_BIND 209 217 ATP (BY SIMILARITY).

```

```
FT BINDING 230 230 ATP (BY SIMILARITY).
FT ACT_SITE 333 333 BY SIMILARITY.
FT DOMAIN 547 550 POLY-SER.
FT DOMAIN 610 618 POLY-THR.
FT DOMAIN 901 908 POLY-ASN.
FT CARBOHYD 55 55 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLNAC. . .) (POTENTIAL).
FT VARIANT 60 60 C -> Y (IN PPH).
FT VARIANT 117 117 /FTid=VAR_013670.
FT VARIANT 117 117 C -> Y (IN PPH).
FT VARIANT 118 118 /FTid=VAR_013671.
FT VARIANT 123 123 C -> W (IN PPH).
FT VARIANT 123 123 /FTid=VAR_013672.
FT VARIANT 123 123 C -> R (IN PPH).
FT VARIANT 123 123 /FTid=VAR_013673.
FT VARIANT 123 123 C -> S (IN PPH).
FT VARIANT 224 224 /FTid=VAR_013674.
FT VARIANT 347 347 E -> D.
FT VARIANT 420 420 /FTid=VAR_013675.
FT VARIANT 483 483 C -> Y (IN PPH).
FT VARIANT 483 483 /FTid=VAR_013676.
FT VARIANT 485 485 C -> R (IN PPH).
FT VARIANT 491 491 /FTid=VAR_013677.
FT VARIANT 491 491 C -> R (IN PPH; SPORADIC).
FT VARIANT 512 512 /FTid=VAR_013678.
FT VARIANT 519 519 D -> G (IN PPH; COMPLETE LOSS OF FUNCTION).
FT VARIANT 828 828 /FTid=VAR_013679.
FT CONFLICT 828 828 R -> Q (IN PPH; SPORADIC).
FT SEQUENCE 1038 AA; 115201 MW; 1389923CE574B913 CRC64;
FT 491 491 /FTid=VAR_013680.
FT 491 491 R -> W (IN PPH).
FT 512 512 /FTid=VAR_013681.
FT 519 512 K -> T (IN PPH).
FT 519 519 /FTid=VAR_013682.
FT 828 828 N -> K (IN PPH).
FT 828 828 /FTid=VAR_013683.
FT CONFLICT 828 828 G -> R (IN REF.1).
FT SEQUENCE 1038 AA; 115201 MW; 1389923CE574B913 CRC64;

Query Match 28.0%; Score 775.5; DB 1; Length 1038;
Best Local Similarity 34.5%; Pred. No. 2.9e-50;
Matches 179; Conservative 103; Mismatches 172; Indels 65; Gaps 19;

Qy 7 LAFVFLISCSGAILGRSETQECLEFFNANWEKDR-----TNQTGVEPCYCDKDKRR 58
Db 14 LPWILLVSTAA-----SQNERLCAFKDPYQDGLGIGESRISHENGITLC----SKGS 64

Qy 59 HCFATWKNISGIEIVKGCWL---DDINCYDRTDCVEKKDSEVY-----FCCCEGNMC 110
Db 65 TCYGLWEKSKGIDNLVKQGCWSHIGDPQECH-YEECVVTTTPPSIQNGTYRFCCCSIDL 123

111 NEKFS-YFPENEVTQPTSNVTPKPPYNN---ILLYSLVPLMLTAGIVICAFWVYRHHKM 166
124 NVNTEFNP-----PPDTPLSP-PHSFNDRDETIIIALASVSVLAVLVALCFGYR---- 173

Qy 167 AYPVLPVTPDGP-----PPPPSLGLKPLQLLEVKARGFCGWKKAQLINNEYVAV 218
Db 174 ---MLTGDRKQGLHSMNMEAAASEPSLDDNLKLLLELIGRGYGVYKGS�DERPVAV 229.

Qy 219 KIFPIQDKQSWNEYEYVSLPGMKHENILOFAGAEKRGTSVD-VDLWLITAFHEKGSLS 277
Db 230 KVSFANRQNFINEKTYRVPVLMEDHNIARFIVGDRVTDAGRMVEYLLVMVEYTPNGSLCK 289

Qy 278 FLKANVYSWNOLCHIAETMARGLAYLHEDIPGLKDHGKPAISHRDIKSKNVLKNNLTAC 337
Db 290 YLSLTSDWSSCRLAHSVYRGLAYLHELTP-RGDHYKPAISHRDLNSRNVLVKNDGTCV 348

Qy 338 IADFGALAKF-----EAGKSAGDTHGQVGTTRYMAPEVLEGAINFQ--RDAFLRIDMYA 389
Db 349 ISDFGLSMRLTGNLRVFGEDNAAISEVGTIRYMAPEVLEGAVNLRCESALKQVDMYA 408

Qy 390 MGLVLWELASRCT--AAGGPVDEMLPFEIEIGQHPSEDMQEVVVHKKRPVLRDYLWQK 447
```

```
Db 409 LGLIYWEIFMRCTDLFPGESVPEYQMAFQTEVGNHPTFEDMQVLVSREKQRPKFPPEANKE 468
Qy 448 HA-GMAMLCETIEECWDHDAEARLSAGCVGERITOMORL 485
Db 469 NSLAVRSLKETIEDCDWDQDAEARLTAQCAERMAELMMI 507

Search completed: May 10, 2003, 18:07:08
Job time : 29 secs
```